employers to the control of the cont	8F976260	23
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NACH dehydrogenize (ubiquinone) Fe-5 protein 7 (20kD) (NADH-coenzyme Q reductase)	BC005954	•
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alche leto reductore family 7, member A3 (fiftatorin aldelivée reductase)	NN 012067	
paptide deformylase-file protein	NM_022341	-
ractom cap binding protein subunit 2, 2010	KM_007362	
IQA0225 probain	AW206115	
amplified in ostaosarcoma	M683900	
Approbational protein FU105-57	AL049795	
putative translation initiation factor	55246436	
2 pungsa saduan dan dan dan dan dan dan dan dan dan d	NM_013366	
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06ADM (Accoba da Ason Nis) box cohrected 8 (RVA helicas)	14 00494	
sia/fitransferae 70 (lapha-N-scarfineuraninyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sia/hitransferase)	A8035172	~
erterogeneous nuclear ribonucleoprotein A3	NM_005758	•
CCAIT/anhancar binding protein (CEBP), garma	NN_001806	~
antino-terrainal archancer of split	NM_001130	~
CG-152 probain	NH_020410	~
mitochondrial ribosomal protein (24	NM_024540	~
scely-Coenzyma A trensporter	NM_004733	~
ATPese, H+ transporting, hysosomal (hacucular proton pump) 940	A862255	.~
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syrvada defrydrogenaze (lipoarride) alpha 1	NM_000284	~
	HH 006289	~
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IVA polymerze Il transciptional regulation mediator (Neds. S. cerevisias, homolog of)	AF074723	~
odynamics (TMA) II (DMA directed) polymericide ( (3340)	AC004382	2.19
uran xila	NM 015963	2.18
067295854011 protein	NH_015416	2.18
34725464611 protein	64289527	2.18
ribohoin 1	U95822	2.18
sypothetical protein MG(3731	NN_024313	2.18
thromosome 11 hypothetical protein ORF4	NM_020155	~

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adaptur-related protein complex 2, alpha 2 subunit	Mazes	
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Breast INA ATP Advanced to the process	NM_000234	2.17
regions, control and control a	8F575514	2.17
sommer sections of many	AB01 1088	2.17
dividitive seminates	030658	2.17
Day (Hep40) homolog, subtamily 6, member 12	NM_017626	2.17
general transcription factor II, i	80004472	2.17
6M2 ganglooxide activator protein	AL513583	2.17
guamine mucleotide binding protein (6 protein), beta polypeptide 1	AF070603	2.16
authoentigen	NM_014329	2.16
RNA binding motif protein BA	COLEGIA	9 5
publishe translation initiation factor	M.337/U/ UM 003764	2 ts
enterpolic translation included factor 3, subunit 5 (epsilon, 4/10)	2020 MM	2 5
Improved protein Net 11.12.7.3. Adv. bear and bearing to a mandage 25 (selection addation) and the bear and the selection of the selection and the selection	NM_003689	2.16
description in the property of	AF109196	2.16
armetin A1	NM_001157	2.16
Albase, H+ transporting, hassomal (nacuolar proton pump) 16t0	M62762	2.16
phosphoprotein regulated by mitogenic pathways	NM_025195	2.16
glutations synthetize	NM_000178	2.16
RNA-binding protein regulatory subunit	NM_007262	2.16
probain phosphalase ZA 48 tiba ngulatory subunit	AC000157	3.16
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standarded order consider 3. defa. 1 submit	AF130042	2.15
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hypothetical protein WGC2718	NM_024067	21.5
(JAA065) protein	NA_014938	5.5
hypothetical protein FLE0312	MA_01//61	21.5
Part (These statements) for the training memory in the company of the training memory is the company of the training memory in the company of	BE379408	2.14
Olf artigon, sidenucin	AF263279	2.14
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Consensus includes gb-AV715578 /FEL=EST (DB_XREF=eg:10797095 /DB_XREF=estAV715578 /CLONE=DCB3B(609 /UC=Hs, 21056 Home statiens cDNA; FU21366 fs, done (DU3012, hig AV715578	, hig AV715578	2.14
postanicki segretation increased 2-like 9	4R/06572	17
A STATE OF THE STA	RG149218	2
prospector of the second of th	NM 004074	213
CAMP anchor attachment protein   homotop (vest)	NM_003801	2.13
hypothetical practein MGC2749	BC006479	2.13
alpha-activitin-2-associated UN protein	AF002280	2.13
membrane metalfo-endeperolduse (neutral endeperplidase, enkephalinase, CALIA (010)	NR_00/28/	5.5
Fortune configuration of the c	NN 016060	2.13
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reproduce province (2.10)	NM_014041	2.13
consultation texture IIII. confunction § (6310)	NM_012087	2.13
seven in absentia homolog 2 (Procophia)	076248	2.13
heterogeneous suchear ribonucleoprotein C (CI/C2)	A4664258	2.13
introgrio-direlaci kinase	NM_004517	<b>6.13</b>

X-ray repair complementing defactive repair in Chinese hamster cells 5 (double-strand-break rejoining; fui autoantigen, 80kB)	104977	2.13
Practin 4	AUJSUSS	3 :
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decaybhaddate tanace (thymidylate tinase)	MR_012145	2 :
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	AA809056	2.12
Addition to the second	8E898639	2.2
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sagral sequence receptor, appra (translocent-us sociated protein alpha)	WO LOCK	;
RAI7, member RAS ancogene tamity	86261416	7
polypyrinidine tract binding protein (heterogenocus nuclear ribonucleoprotein I)	NM_002819	5
simplitunisterae 9 (CMP-Neukchetosykenamide ajsha-2,3-sia)ttransferase; 6M3 synthase)	NN_003896	2.13
IDMO164 gene product	BE963370	<b>=</b>
BRCA1 associated protein	AF035620	7.
Helizabeth Landenna	NM 018848	7.1
The second state of the second	RC004383	2.11
purply principles were a many of purple systems in the control of	AF300650	2.11
Specimen increases a naturally broken (a process) of	A1375486	2.10
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chrc finger protein 22 (KDX 15)	AA/44//I	2 ;
WOLIN protein	ALCO4045	2 :
microbulule-associated protein 4	NM_002375	5.10
acid phosphatase 1, solubble	NM_004300	2.10
dolidnyk-phosphute menosyftzansferzse polypeptide 3	NM_018973	23
ghuzza regulatied protein, 58tD	083485	2
DEAD/N (Asp-Gu-Ne-Asp/Nis) box potypoptide 3	Recoes	8:
pyravate dehydrogenase (lipoamids) beta	H34055	2.09
prefolds 2	NH_012394	8
profine synthetase co-transcribed (bacterial homolog)	AL 136616	2.09
majabbor of COXA	NM_006067	8
mohfodenum cofactor synthesis 2	NM_004531	23
El-donnain containing 1	AF001434	8
Prypotherical protein FU21324	NH_021941	8
phosphothuctophose, liver	NM_002626	5.03 7.03
spectrin, alpha, non-enythrocybis 1 (alpha-hodrin)	U83867	8
GALFO2213.2.1 (DEF #Homa supiems PANZ mRNA, complete cds. /FEL=mRNA. (PROD=FANZ /DB_XREF=gi:5138913 /UG=Hs.284275 Homa supiems PANZ mRNA, complete cds. /FEL=gb./FO91.4709.132	39; AF092132	<b>607</b>
calcium binding protein (4045 precursor	NM_016547	2°
growth tactor, augmenter of lever regeneration (ERV1 homelog, S. cerevisiae)	AF124604	8
Rho-specific guanine nucleotide exchange lactor p114	AB011093	80.7
zinc finger protein 289, (01 regulated	BE299671	2.08
up-regulated by MG-CWS	AL049963	208
hypothetical protein FU12542	NM_024899	2. 2.
KDA0872 protein	M629033	2.03
low molecular mass ubiquinone-binding protein (9.540)	NM_014402	88
transcription factor 0p-1	R60866	80.2
(IEBP/EF300 inhibitory protein 1	A-1098/3	8 5
guarine nedeotide binding protein (6 protein), beta 5	MM_0065/8	9 5
hypothetical protein	K310//	3 5
hypothetical protein F1120758	NM_017952	707
D6724341154 protein	MM_016003	63 5
phosphorbonydychamide formyfiranstwasa, phosphorbosylgycmanide synthetae, phosphorbosylamnoimidazne synthetae	KM_WW819	3 5
GENERAL PRESENCE OF THE PROPERTY STATES TO THE PRODUCT OF THE PROPERTY OF THE	24 8(UVI233	3 5
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hypothetical protein FLI20607	NM_01/899	7

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2 BECONCIA DOSINONI PROMININA	A4126728	90.7
Hoodean common Burkel	AF151056	5.06
Migratuse-essociated protein like achinodem EHAP	AISB2285	90.7
CONSISTED INCHES 90:3F037323 /FEA=EST /08_XREF=g:10746209 /08_XREF=est 60146199471 //LONE=IMAGE:3865487 /UE=Hs.9683 Dnal (Hsp40) homolog, subtainity C, ment	er 3 BF037823	5.06
polyanere-modulated factor 1	NM 007221	5.06
progestin induced protein	AF006010	8
tumor differentially expressed 1	RCOOCUEE	3 2
SET translocation (meeting lautemia-associated)	1170000	8 3
orthasome (orthone, marranain) 265 subusit Ann ATD see 13	MC/8616	8 :
and the name of th	NM_00281/	90.7
P.R.C.	NM_003099	<b>5</b> .06
No.2.4; memoer IAO Grouper Lamin	NM_004162	90.7
best when apper transcription lactor, ATF-like	AC007182	5.06
pfluitary tumor-transforming 1 interacting protein	NM 004339	90
sialidase 1 (prosooma slaidase)	37/2481	2
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recommendation of the second o	U34074	5.05
	AF230401	5.05
A CONTROL OF THE PROPERTY OF T	NM_006134	2.05
tabouan, apha 1 (testo specific)	ALS65074	2.05
estylphorone phosphate shufture	KM_003659	2.05
FUS interacting protein (serine-erginine rich) 2	AU130523	2.05
hypothetical protein M622491	NM 024040	2.05
Pysyl-dRMs synthetase	AF285758	502
Clp1-interacting zinc finger protein	AA054734	5
problem tyroxine phosphataes, non-receptor type 22 (fyrrachoid)	NM OTFOCT	3 6
emodetarse (style-terodetarse) dehydrocense (finounde)	WW 003541	6.6
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Typochadical protein Pull 183	NM_018351	<b>*</b> 0%
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	NN_015367	2.03
A class I region expressed give KZ	NM_014260	2.03
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standy-Los desaurase (onta-9-desaurase)	A678241	2.03
estra strongenous control	NM_006556	2.03
BOSKUULOS), 1 / URF #HOMO SUPPERS, COMP NEL 31 BZ, MANA, COMPIECE CES. / FEA=MRNA / PROD=UNKnown (protein for NEC.31 BZ) / OB_XREF=9:12653008 / UG=Hs. 315417 Homo supie	ns 8C000265	2.03
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reinchondrial ribosomal protein L42	04) 25(45) WM 017975	
Applications of process in the control of the contr	HM 006224	
definement and basis established programmed to the control of the	NM_014316	
SCOTT COLUMN	NM_016096	
23/52 protein	NM_016565	
pdymamae (DNA directed), delta 1, catalytic subunit (12540)	169200_NN	
ypothetical protein	2E6510_MN	
CD74 antigan (invariant polypaptide of major histocompatibility complex, class II antigen-associated)	XPL10X	
-etbooystransferrase (NAD+; poly (ADF-ribose) polymerase) tike 1	AL359763	
Consenses includes gb./L.109942 /DEF = Human DNA sequence from clone RP3-4/3116 on chromosome 6q25.3-26 Contains 3 end of the RAV31A (mitogen-activated protein kinase kinase ki		
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methorithe adenosyttanstierase II, alpha	LISCON MA	
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hypothetical protein PT2447	SOCCEON NA	
preferant transferance complete beta	MH DOEA17	
P-ert sertorin ("Schmid-Luppin A-L) viral ontogene nomotog (avan)	783000AF	
Typothetical protein FLI22104	AUCODE 411	
ncatyl-Coenzyme A ecutyltranstense 1 (acetoacetyl Coenzyme A thiolase)	61000-MM	
Jycard-3-phosphata dehydrogenase 2 (mtochondria)	016960	
guanisinoscelata N-methyfransferso	9C1000 WK	
temor necrosis factor (ligand) superfamity, member 8	NM_001244	
al Abelson exurine textremia viral concepture homotog 1	NN_005157	
adypartmidine tract binding protein (heterogeneous nuclear ribonucleoprotein i)	BC002397	
shooplodiesternse 44, cMP-specific (phosphodiesterse E2 dance homolog, Drosophila)	NM_006202	
100 100 to the contract of the	AK001363	
Conserved by AV002076.   DEF = Home series cDNA FULL214 fis. close PLACE 1007990. FEA=mRNA /DB. XREF = ci.7023738 /UG=Hs. 281616 Home series cDNA FULL214 fis.		
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high-mobility group (nonhistone chromosomal) protein 17-like 3	NM_006353	
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sell membrane dycoprotein, 110000M (r) (surface antigen)	MM_007002	
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December cretain \$10	AA320764	
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morel combyme A hydratizes, short chain, 1, mitochondrial	26200-PM	
MAOSTI protein	SECTION MIN	
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othetical protein FU13057 similar to germ cell-less	NM_0624/1	
RAMONO gene product	1/9953	
probasoma (prosome, macropain) activator subunit 2 (PA28 beta)	818200_878	
IAM binding protein 7	AA939270	
prestatic binding protein	1269631	
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	DM binding motif protein SA	M738479	
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GPC156 problem	NM 014178	
ow density lipoprotein receptor defect C complementing	NM 007357	2
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DRIDM (Kep-Gh-Ma-AspAfis) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; feukophysin)	BE561014	1.89
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general transcription factor (IP), polypeptide 1 (62/td subunit)	MM_005318	9 5
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SMC structural maintenance of chromosomes 2-like I (yeast)	KM_006444	79.
ATPeas, aminophosphologid transporter (APLT), Class I, type 8A, member I	AB013434	1.8/
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nuclear factor (enythroid-derived 2)-libs 2	NM_006164	7
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Consensus includes go.XN073564 /F6A=EST /D8_XREF=gi:8007617 /D8_XREF=est:ho62c10.11 /CLONE=INAGE:3041970 /U6=Hs.155485 huntingin interacting protein 2	AW873564	1.84
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esydem, light polypaptide, regulatory, non-sarcomenc (20kD)	NM_006471	28.
discripty corrol O-exystrans ferrors homolog 1 (mouse)	KM_012079	3.
protein phosphatase 2A, regulatory subunit 6" (PR 53)	NM_021131	28.1
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high-mobility group (nonhistone chromosomal) protein 17-like 3		28.
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golg SWV receptor complex member 1	NM_004871	3.2
phospheticy/serine receptor	AK021780	28.
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Gene with multiple splice variants near HD locus on 4616.3	NM_003704	1.82
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hypothetical protein FLI22175	AA551370	1.79
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polymerze (RW) III (DW drecked) (62k0)	193867	67.
probazione (prosone, mempain) 265 subunit, non-ATP 2se, 7 (Hox34 homolog)	NM 002811	2
photosi-12-mytistate-13-acetate-induced protein 1	A857639	62.1
60t5 general control of amino-acid synthesis S-like 2 (ye.st)	NM 021078	1.79
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isotom 3	NM 001689	1.79
Hela cyclin-dependent lixuse 2 interacting protein	NM_016550	1.79
cytochrome c axidese subunit Vilb pseudogene 1	AF042164	1.78
thyroid homone receptor interactor 8	M694023	1.78
similar to Caenorhabditis elegans protein (42(1.9	ALS68449	1.78
Exerciting or protoun 95 homolog (mouse)	0F196931	1.78
uraci (SZMM)	AK025504	1.78
Carly Sharehold (F. connection)	NM_004290	1.78
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ATP ase, IH+ transporting, lysosomal (recoolar proton pump), member 1	BC003564	1.78
sertuan selecti matrix flye information regulation 2 homolog 7 (5. cerevisiae)	NN_016538	1.78
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chromosome 11 Propoductical protein ORF3	NN_020154	<u>.</u>
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hypothetical protein FL13194	KR_U25146	3
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receptor (TIGRSF)-interacting serine-threonine kinase 1	1,50062	1.63
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IQVA778 protein	A1798790	8
\$\text{90.1K002361.1 \(\text{OEF} = \text{Months expires}\), \$\text{Similar to transducin (beta)-like 3, clone \(\text{MC.1615}\), \(\text{MR.N.}\) complete cds. \(\text{FE} = \text{MR.N.}\) \(\text{PROD=Similar to transducin (beta)-like 3, clone \(\text{MC.1615}\), \(\text{MC.1617}\) and \(\text{MC.1617}\).	80002361	3
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IQVO978 protein	N64780 1.6	8
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probability rocaine bhase 9		9
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Chaperonin containing (CVI suburit 2 (beta)	NM_006431 1.60	9
south carrier throwy 35 (UDF-H-wellyfightcocharine (UDF-Gick/kc) transporter), member 3	NA_012243 1.60	9
NUCHA INCINIZATION SUGNAL OPEREZA IN VENOCAMBOTIONA SYNCTOME	NM_003776 1.60	9

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NN 015646	53
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NM_018107	1.59
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AF040105	1.59
AL050147	£. 5
NM_001023	<u> </u>
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NM_015909	1.59
9000039	1.59
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BC002703	1.59
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NM 006858	1.59
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NM_015324	3.
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hypothetical protein FUZZ-405	AY007098	1098	33.
XXI Suppressor of RNA polymerase 8 homolog (yeast)	046837	73	33.
LAWD642 protein	A8020649	649	33.
cargo selection protein (mannose 6 phosphate receptor binding protein)	NM 005817	05817	85
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Consensus would go AL 13428 / UNE Thuman UNA sequence from clone RPS-1071L10 on chromosome 20 Contains part of a gene for a new member of the thymosininterferon-inducible m	te thymosininterferon-inducible m AL133228	228	<b>3</b> 7.
hypothetical protein FL20568	A436930	930	<b>3</b> 2.
hypothetical protein FU10241	A768100	8	1.58
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State of Settleties (Institute of Settleties	KM_00035	10351	2
hypothetical protein FLI12553	NH_024700	54700	<u>-</u>
Zinc metalloproteinase (STE24 homolog, yeast)	NM_005857	28857	<b>3</b> 7
thiosuffice suffertransferace (rhodamese)	D87292	~	<u>.</u>
protein kinase, interferon-inducible double stranded RNA dependent activator	AF083033	033	37
Derber of RAC1 (artacin 2)	NM 012402	2402	5
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7 Labour Bloom	MM_006603	26603	2
NUM 1356 protein	AL080102	20	.58
hypothetical protein FU20011	80003086	086	<b>8</b> 5
p47 protein	NM_018839	18839	<b>3</b> 5.
DKT2P564H082 protein	NM 014042	4042	25.
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second mitochondria-derived activator of cuspese	NM_019887	9887	25.
ribosomal protein 517	BF026595	295	25.1
H4 histone tanily, member E	NM_021968	1968	1.58
Consentus includes gb:8E539424 /FEA=E51 /DB_XREF=gi:9761069 /DB_XREF=et:601068256F1 /KLONE=INMEE:3454693 /UG=H9.283283 Homo supiens cDNV: FU22335 fs., chone HRti	s cDNA: FU22355 fis, clone HRC: 8E538424	154	35.
feritin, heavy potypoptide pseudogene 1	104755		25
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moment polyphonograms — prosphatos (type I, 10/10)	NM_00402	4027	
inhighn, beta 1 (horometin receptor, beta polypeptide, antigen (D29 includes MDF2, MSK12)	AA215854	<b>3</b>	1.57
phosphogucomutase i	NM_002633	5633	1.57
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SWIAM related matrix associated actin december resolutor of chromatin, subfamily a member 2	AV725365		25
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mitochandrial ribosamul protein L46	NM_022163	1.57
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phosphortuctolaines, liver	80006422	1.57
calcinear'n binding protein 1	AB002328	1.57
DEADA (Academalana Aria) ban nobrancida S (RNA belinne 880)	NH 004396	1.57
The state of the s	WM O16281	0
ACTIVITY OF STREET	1070107111	} 5
MANUAL DESCRIPTION OF THE PROPERTY OF THE PROP	ALS46600	<u>ر</u>
IDEL (1/3-449-612-Lou) endoptasme reticulum protein retention receptor 2	ALS42253	.5
mannose P-dothol utilization defect 1	AF059752	1.57
RAD22 homolog A (S. cerenisies)	NM_005053	1.57
Immediation protein 61/21/212	NM 024642	1.57
All thought in the feet and also	D31885	5
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programmed cell death 5	NM_004/08	<u> </u>
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Prypothetical protein FLL20561	NM_017882	25.
ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	AB017644	95.1
hardholdin interaction proteins 1 -related	AB014555	25.
That Markett bounded address to	NM ONSS28	5
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TITLE OF THE PROPERTY OF THE P	AL13513	R :
ON-U-STILL PROCESS	ABU28828	8 1
confrommer protein A (17AD)	NM_001809	*
phospholipase C. garren 1 (formerly subtype 148)	AL022394	.S.
centaurin, beta 1	NM_014716	35.
karyopharin (imports) beta 1	BC003572	35.
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Conservate includes of ALS 15874 FEBA=57 AB XREE=cr.12779367 AB XREE=cr.48 518874 At ONE=CXORAGO17FOG (3 prime) ALG=Hs, 83066 Home sazions GT212 mRNA	ALS15874	1.56
iderauth 2-sulfatese (Purter sendrome)	NM 000202	1.56
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Lank (bectarial lantiblotic synthetase component ()-like 2	NM_018697	8
redeoporin-like protein 1	NM_007342	35.
hypothetical protein FU20477	AA203365	35. 25.
activity, apple 4	U48734	8
CDC5 call deksion cycle 5-like (5, pombe)	AW268817	35.
APG12 autophagy 12-tite (S. cerevisies)	8E965998	8.
NS1-binding protein	AB020657	<b>3</b> 5.
FQAAQ24 protein	NM_015136	95.
similar to vaccinia vinus Hindill K4L ORF	NM_012268	<b>3</b> 5.
Consensus Includes gb: \$E830828  FEA=E57   DB_XREF = gi:10329604   DB_XREF = est:601493261F1   /TLONE = IMAGE:3895407   /U6=Hs:84775 Human transposon-like element mRNA	8E880828	<b>3</b> 5
hatenin p80 (WD40-containing) subunit 8 1	NM_005886	25.
hypothetical protein FU11249	KM_024591	35.1
acide protein rich in laucines	NM_006401	95.
regulator of 6-ordain signalling 14	AF037195	95.
hetenogeneous nuclear ribonucleoprotein U (scatfold attachment factor A)	BC003621	1.55
eutaryolic translation initiation factor 28, subunit 3 (sammu, 58kD)	NM_020365	1.55
beside (OK blood group)	ALSS0657	1.55
hypothetical protein FL20729	KM_017953	1.55
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hypothetical protein FU10101	BC002142	55
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hypothetical protein FU10808	1010 MM	3 5
hypothetical protein FU20373	367710 WW	
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serine hydroxymethyftranse 2 (mitochondrial)	A1770514	3 5
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contrast contrales, subunit abba	AI621079	<u>z</u>
OK 13 protein	NM_020188	<u>.</u>
phosphaticse and tensis homolog (mutated in multiple advanced cancers 1), pseudogene 1	AF023139	<b>3</b>
IQAA0729 protein	A8018272	<u> </u>
idurante 2-suffatase (Punter syndrome)	NM_006123	<u> </u>
encochallar-associated protein 2	NA_01/439	Ķ
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major follocompatiblistic complex, class I-skie sequence	NM 021052	Ž
ACA Included parameter and an academy and academy	031815	3.
INDUCATED IN SECURITY OF THE PROPERTY OF	NM_001006	35.7
the control of the co	AK024386	7.
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boogary Contryme A dehydrogenese	AX022777	3
hypothetical protein PU12448	NM_022895	<u> </u>
MCM4 minichromosome maintenance deficient 4 (5. cerevisite)	A1936566	<u> </u>
perceisomal short-chain alcohol dehydrogenase	NA 021004	X :
hypothetical protein MGZ-463	NM_0240/0	<u> </u>
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and popular (layer and popular)	AF062483	<u> </u>
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Appendix (ACC)   Appe	PARTY CASE 1119 amobile	AL050102	¥.
MM_00182  MM_0139940  MM_0139940  MM_01393941  MM_0139371  MM_0139371  MM_0138371  MM_0138371  MM_0138371  MM_014771  MM_017774  MM_	Companies includes challe 293594 FELH=EST (OB, XREF =q; 11685918 /OB, XREF =q; 7412408 x1 /K104KE=11MAE; 3697839 /UIC=Hs. 274440 Nomo sapiens mRNA; c01	A DKF2p4341139 (fr. 8FS93594	7.
MM, 1019940 MS, 172 MR, 128159 MG, 1018222 MR, 1018222 MR, 1018222 MR, 1018222 MR, 1018222 MR, 1018223 MR, 1018223 MR, 101823 MR, 101823 MR, 101823 MR, 101823 MR, 101824 MR, 101826 MR, 101826 MR, 101826 MR, 101827 MR, 101827 MR, 101827 MR, 101828	adactor-related proxim complex 2, beta 1 subunit	NM_001282	<u>z</u>
M464313  M464313  M464313  M464313  M464313  M4,001055  M4,001322  M4,001323  M4,001333  M4,001343  M4,001343  M4,001343  M4,001343  M4,001344	Prypothetical protein M6(4276 similar to (48198	NM_030940	<u>.</u>
MAT18159  Ad442913  Ad442913  Ad442913  Ad442913  Ad1, 101222  Ad1, 101222  Ad1, 101233  Ad1, 101233  Ad1, 101343  Ad1, 101343  Ad1, 101343  Ad1, 101434  Ad1, 101343  Ad1, 101434  Ad1, 101434  Ad1, 101343  Ad1, 101438  Ad1, 101338  Ad1, 101438  Ad2, 101438  Ad3, 10	green, light cohraction 4, aftall arial embronic	M36172	<u>3</u>
M. M. A. M. M. LOO1055  2. (T-cell specific, HMC A999-9687  M. LOO10322  M. LOO10322  M. LOO10323  M. LOO10333  M. LOO10333  M. LOO10333  M. LOO10334  M. LOO10334  M. LOO1034  M. LOO0038  M. LOO0038  M. LOO0033  M. LOONOS3	H3 Metons, family 38 (13.38)	AW138159	7
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251 Far precific, 1916, A194-012222 NHL, 2013867	aufternacionae family, cytosofie (A chenologicalism) member (	NM_001055	<u>.</u>
M. (201222) M. (201382) M. (201382) M. (201382) M. (201382) M. (201382) M. (201384) M. (2013854)	Consumers included to AND	(T-cell specific, HMG A)949687	<u>.</u>
M. (201983) M. (2019867) M. (2019867) M. (2019867) M. (2019862) M. (2019867) M. (2019867) M. (2019867) M. (2019867) M. (2019867) M. (201987) M. (2019887) M. (201987) M. (2019887) M. (2	must' homotoo (E. cofi)	NM_012222	<u>.</u>
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M. (1) 6821 M. (1) 6821 M. (1) 6823 M. (1) 682 M. (1) 13 662 M. (1) 13 6	putative neurodranamitier receptor	NM_003967	1.53
251 Rar protein Matal Madd 141  Mil 201477  Mil 201477  Mil 201477  Mil 201478  Mil 201477  Mil 201478  Mil 201578	omactin 4 (ps2)	NM_016221	1.53
M.1.0233 M.1.0233 M.1.0233 M.1.01804 M.1.01804 M.1.01804 M.1.01804 M.1.01804 M.1.01806 M.1.01806 M.1.01806 M.1.01806 M.1.01806 M.1.01806 M.1.00306	Consensus includes gb.M344141 /FEA=EST /DB_XREF=gi-4081347 /DB_XREF=est:tc02do9.x1 /CLONE=IMAGE:2062673 /UG=Hs.Z29850 ESTs, Highly similar to 6015	51 Rar protein H.sapi A344141	 
H. J. 1806.2 H. J. 1806.2 H. J. 1917.63 H. J	1QAA0090 protein	A1143233	1.53
MY_0.19862 WY_0.19862 WY_0.19863 WY_0.19747 WY_0.197233 WY_0.29311 WY_0.29312 WY_0.29312 WY_0.29322	ADP-reboxylation factor 3	M33384	1.53
M. (2011) W. (20	Proothetical protein FU10335	NM_018062	6.53
MY (2011) 63 MY (2011) 10 MY (2011) 10 MY (2011) 10 MY (2012) 11 MY (2018) 11 MY (2	(IAA0237 enne product	NM_014747	1.53
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MUL 203425  MUL 203425  MUL 203425  MUL 203425  MUL 203426  MUL 203426  MUL 203511  MUL 203428  MUL 203513  MUL 203521  MUL 203524	Startin B. beta (acto binding protein 278)	AV712733	1.53
HN, 003425  L25511  HN, 015976  HN, 015976  HN, 015976  HN, 000188  HN, 0100188  HN, 0100188  HN, 0100188  HN, 0100188  HN, 000188	DR729560,0724 protein	AU158148	1.53
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MH_017554  MM_0005807  AL120741  AL120741  MM_000180  MM_000180  MM_017743  MM_017743  MM_017743  MM_017743  MM_0003754  MM_0003754  MM_000380  MM_017348  MM_017348  MM_017348  MM_017348  MM_017348  MM_017348  MM_017358	sorting natin 7	NM_015976	1.53
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##	human homolog of Orosophila Scribble	A469403	1.53
HY (2001 88) HY (2001 89) HY (2	iemunoglobulin heavy constant mu	86340670	1.53
Mil.   17732   Mil.   177322   Mil.   177	Nexodinase 1	NM_000188	3.5
AM-27090 AM-17090 AM-17090 AM-17090 AM-100356 AM-200356 AM-200359 AM-200559 AM-200559 AM-200559	hypothetical protain DC 42	NM_030321	3
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Wi_224910	sparvers across a very poor season a very season se	AF256223	1.53
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MH_011438	ubiquitis-conjugating enzyme E2N (USC13 homolog, yesst)	NM_003348	3.
A	KIAA0837 gene product	NM_014838	2 (
propried 5  frieds2023	ubiquitis fusion degradation 1 like	900000	ב יַּ
ang protein 2 AC002310	UDF-Catherial (KNk Defa 1, 4, galactosyfitansferase, polypopide 5	ALU35063	¥ 2
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NA_000308	cytoplasmic polyadenylation element binding protein	NM_030594	3.
10,0004 N1,025,04 N1,053,03 N1,054,03 N1,055,3 N1,055,3 N1,055,3 N1,055,3 N1,055,3 N1,055,3 N1,055,3 N1,055,3	protective protein for beta-gulactosidase (galactosialidosis)	NM_000308	<u> </u>
M-0.2526 HI-0.2526 HI-0.2526 M-0.2529 M-0.2529 M-0.2523 M-0.2523	activ, beta	D20604	¥ 5
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als MGC(19963) Acceptabilise type IVA member 2	Therefore the control of the control	N139569	3.
	STREET OF PROMISE Incompletely of provide INCC (1963)	NM_030573	3,
	replace through process (A. member 2	AF208850	3.
	et property of the state of the	A8000263	ž

hypothetical protein FU13912	NM_022770	3.1
(SNG) and IT building protein	W84482	1.52
The model from the	AW471220	3.
manney (appel -) - Spreadonan orde 1, c-n-actyglicosaminyttansterace	AW103265	3
And estimated problems	NM_012245	3.
INTERNATIONAL CONTRACTOR TO THE SECURIOR SECURIO	NM_006221	2
hereafted in results (1) DOCCAS	NM_004804	χ.
trave specific fransplantation anticen #358	KM_01/900	χ:
hemochromatosis	AF115564	<u> </u>
HWV-1 Tat interactive produin, 60 kDa	NM 006388	2
PQ2-entagonist of call dearth	066879	3.
hypodentical protein PR01550	NM_018502	3.1
N.Z. Bastone family, member F	NH_021062	3.
1117 General Particular and California and Californ	NM_006303	3.
regime recognitions particle (F. Conferencial et al. 7440 automatics).	BE856385	5
y general extension (17 mg and 17 mg	AW190445	5. 5
tresie insering	NM MODES	5 5
IOMO244 protein	85430956	
\$\text{gham_005703.2}\$ \tag{APR_005703.2}\$ \tag{APR_005122}\$ \tag{APR_005703}\$	/DB NM 005703	15.
I complex 1	8000065	-5.
CTT1 protein	NM_020151	15.1
ukiquithr proteim isopeptide ligase (E3)	NM_014671	1.51
Rayophan (megalia)	6000947	1.51
UV-IL-SOS INC. PETERS Publish had a company of the	NM_015537	<u>.</u>
III merentra adapte contain	NA_001069	5.5
Production contain [114:53	WIBS/60	5 5
professione (procons, nacropale) subunit, beta type, \$	RCD04146	2
interferon, germa-inducible protein 30	NM 006332	15.1
hypothetical protein FU2003	80005212	1.51
SAME protein	NM_006555	1.51
prognownose - Johnson 4 prognetiony subunit 4, p1 50	BF740111	1.51
Form William (1904)	AF062347	5.5
(Gally brenden	MM_016628	<u>.</u>
polymerze (RWJ, II (DNA drected) polypeptide ( 13340)	Al224143	5 5
VAMP (vesicle-ussociated membrane protein) -ussociated protein A (3340)	AF154847	5
hypothetical protein FL20596	AF336851	1.51
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pouzavien volgegiggige of memore, some view of some some some some some some some some	NM_004979	
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DELOM (No-dia-Na-Ara) has polypepide 9 (RNA helicase A nuclear DNA helicase II: leukophysin)	NM 001357	5 5
karyopheris beta Zi, transportin	66258639	1.51
gyrogen symbase 1 (marde)	NM_002103	1.51
LAMAZE POTENT	AB006624	1.51
The action of the second of th	NM_002157	15.1
Security of the security of th	B(000354	5.5
TAX1-binding protein 2	AF241230	<u> </u>
eadaryotic translation elengation factor 1 epsilon 1	NM 004280	5
hypothetical protein MG3180	NM_024041	1.51
verb-b2 enthroblests; teletima and encogene homolog 2, neurolgitotisationa derived ontrogene homolog (evian)	X03363	1.51
emogen-extrained protein three fittings ?	AW007458	15.1
s, et communication on manner mengeschen staten og gette. Psycological proteins (1) 1561 5 similar to membrane nordnin culturised at MARCHIK ACS culturanish membran 51	KM_006515	1.51
Propobacius protein FU11164	NM 018346	3 5
H4 histone family, member D	NN 003541	<u> </u>
atazia telangiactasia mutated (inchules complementation groups A.C and D.)	U82828	8
habiting with who will also as a second of the second of t	80006481	3.50
(UMU799) protein	A8023216	<b>95.</b>

DEADA (Men-Ele-Ma-AtanAta) bar cohrection (6	136997	
Promise to the state of the state of the second control of the sec	NM CO1530	
probasom (procoms, mercosin) 265 subunit, non-AlPase, 1	NN 002807	
hypothetical protein FL10583	NM 018148	3
hypothetical protein FU10814	NN 018230	_
KJW0399 errelwin	NN 015113	_
Proofbatical protein similar to beta-transducin family	SPORTO MA	•
dCHP dearnings	80001286	_
medizzin 1	RC001906	-
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NH 002166	_
hypothetical protein MGC2745	NM 024117	_
Consensus includes ab.AW138902 /FEA=E57 /08 XXEF = ai 61 43220 /08 XXEF = est UI ++ 811 - sea = - 08 -0- UI = 1 XLONE = IMAE 2720342 / UIS = H. 173108 Homo suriens CDNF EL121897 6 AW138907	Diens cDNA: FU21897 6 AW138902	_
caldum/talmodulin-dependent protein kinase I	NM 003656	_
entrachondrial Import receptor Tom22	NM_020243	
AJA0998 protein	A8023215	_
NO kinase	Al334128	-
cacherin, E6f LMs seven-pass 6-type receptor 1 (flaminos homotos, Droscobilia)	8000059	-
west marke sercens 3611 viral encourse homeloo 1	759100 WW	-
RAN binding protein 2	D42063	-
tyrosine 3-monocaygenase/Dyptophan 5-monocaygenase activation protein, beta polypeptide	BC001359	_
coated vesicle membrane protein	NH_006815	
alamine-glyonylate aminotransferase (ozakosis I; hyperozaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	013368	
RA868, member RAS oncogene family	BC002510	
hypothetical protein ME(10940	80004331	-
Down syndrome critical region gene 2	NM_003720	-
hypothetical protein	MM 015705	
KDAD515 protein	A/026025	_
MC23 protein	NM 025259	
mittogen-extivated protein these timese kinase 7	NH 003188	_
ets verlant gene 5 (ets-related molecule)	BF060791	_
Consensus includes Ob Fallomo sapiens CKCR4 gene encoding neceptor CKCR4 /FEA=mBNA //DB XREF=qi:3059119 /UG=Hs. 89414 chemokine (C.X.C motif), receptor 4 (fusin	notif), receptor 4 (fusin Al224869	_
chromobou homolog 1 (NP1 beta homolog Drosophila)	NM_006807	
nuckeoporin 62k0	NM_012346	-
programmed cell cleach 2	NM_002598	-
hypothetical protein FU12171	NM_024619	_
CD22 antigen	X59350	-
adenylate kinase 2	AL513611	=
Rayophern (importin) beta i	86545463	=
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acidic protein rich in leucines	AV712577	-
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And the processing of the state	AA868332	⊒ 1
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MARY TO THE STATE OF THE STATE	NM_024815	-
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inductional profession Se finance 9 0000, poppeduce 1	NM_002953	6.49
(stiss) a gramma, gamma c (setts)	NM_000294	64.
meanant protein 2	KM_002518	1.49
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MALZAGENOWIŁE E I SIZU MENEZDIĄ protein	NM_013978	1.49
protessome (protoms, encropaer) 265 suburid, ATP.ese, 2	NM_002803	1.49
XT bristocation (myeloid leutema-essociated)	NM_003011	1.49
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:	86391005	<b>\$</b> :
Casen Makes 2, april   polypoptide	KM_001895	1.49
CAZ+-promoted Also manthe and	NM_006989	1.49
hypothetia protein FU1547	AL049319	1.49
hypothetical protein MicLobol	NM_030914	-49
print, desmosome associated protein	AW152664	 
problem phosphatose 2A regulatory subunit B' (PR 53)	X86428	1,49
(UNCAS) protein	NM_014941	1,49
metry/fibricaciencesine phosphory/Loe	AF 109294	<del></del>
hypothetical protein FU13909	NM_025108	1.49
IABAN member IAS ancagene lamily	NM_002869	1.49
coffagen, type IV, styha 3 (Goodpasture antigen) binding protein	KM_005713	1.49
Alg.S. S. carevisiae, homolog of	NM_013338	1.49
benzodazprine receptor (peripheral)	NM 000714	1.49
zinc ffinger protein, subhamily 1.A. I (likarus)	580876	67.
displaneas homolog 1 (Drasophia)	All: 58818	5
ADP-ribosytransferase (NAD+; poly (ADP-ribosa) polymerase)-like 2	Al236912	9
Consensus includes gb: AA001552 /FEL=EST /DB_XREF=gi: 1437017 /DB_XREF=eritze-46c:08.s1 /CLONE=IHAGE:362030 /U6=H5.59839 ESTs, Weakly similar to CGHU7L colladorn alpha 1 (III AA001552	1 (III AA001552	1.49
dhydroprimidinas-like 4	AW090187	1.49
regulator of 6-protein signalling 16	094829	1.49
Consensus includes gb:H74089.1 / DEF = Human TB1 gene mRNA, 3 end. /FEA=mRNA //ER=TB1 / DB_XREF=gi:182400 /UG=H9.75639 Human TB1 gene mRNA, 3 end	M74089	1.49
sorting each 17	NM_014748	1.49
IQAA0683 gene product	A8014583	1.49
KUAA258 gene product	NM_014785	1.49
arimodevalisate, detta-, synthase 1	NM_000688	1.48
hypothetical protein FL10509	NM_018119	1.48
breteldin A-britished guanine mudeotide-cachange protein 2	AV657604	1.48
inosine triphosphatase (nadeoxide triphosphatae pyrophatase)	AF219116	1.48
ribosomii protein S4, X-linkad	AL035603	1.48
cyclin-dependent kinase (IOQ-iiia) 10	AF153430	<b>34</b> .
COMMITTAIN INCLOSES (FLAESS TOB) AREY = 91.12677.362 (OB) AREY = est-602323331F1 (CLONE = IMAGE: 4426926 (UG=H3.226138 Homo sapiens mRIN; CDNA DIYZPSG6H2.44		84.
STULLED IN CONTRACT OF THE PROPERTY OF THE PRO	NM_004718	<b>.</b>
reprometure protection of the biodica t	40/470 EX	<b>9</b> :
Superior processing ()	MA_W234	2
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protection of telenares 1	80002923	- -
protein kinese, AMP-activated, beta 1 non-catalytic subunit	KM_006253	1.48
serviciocially defined breast cancer artigen 84	AF091085	1,48
ElS interacting protein (serine-arginine rich) 1	NM_006625	1.48
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Negriptingcoine emdothytholase (act ceremidase) title	NW DOSA71	3
Myears, light polypaptide, regulationy, non-sarroment (2010)	NA 000701	
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IQAA069) protein	M300K33	
dacytypred these, ask (1040)	MM_W3940	2 5
hypothetical protein 018 tp 5640023	Alltanda	3
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hypothetical protein FUT 3441	MW 017901	2
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CONSTRUCTION OF A CONTROL OF A	NM 025241	27
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the property of the state of th	A15,66096	
putable DIAA briding protein	1,0200 MM	3
hypothetical protein PUI 3117	NM 022719	5
Descripe syndrome critical region gene DALI, lakely ortholog or mouse expressed sequence a emoryonic terms	WGOGSG	2
weace translang, baach and anchor containing	NW COSS33	2
Molecytechronia c symbols (cytodromic c herne-lyske)	NW OTRIGI	3
hypothetical protein FU10540	44047334	7
crititate describayisse entayre inhibitor	NW ONSTREE	3
estanyote transmon intainon factor 4, subunit ( [Zeta, eo/o/tu]	NM 002156	4
heat shock both protein 1 (chaperonin)	NH 003993	1.47
CON-Marie Entrare C	AA478965	1.47
METATACHE MANAGEM I HER I	NH 018129	4
Production product to 110335	AF155159	4
adaption-whited protein compart 4, sigma 1 subunit	44886971	1.47
MYC I ad interactive protein, 60 kJ/a	726100 MM	0
	NM 004818	1.47
PICE OF STATE OF THE STATE OF T	A1220627	1.47
E have been seen and the seen a	NM 012175	1.47
T-SE CHAPTER STATE THE PAGEST 1 MF = Nove capture mRNA: - CHAPTER SEAF 112 (from close DRF20564F112). FEA=mRNA / DB 78FF = 01-4884238 / UG=Hs. 166361 Homo sapiens mf ALO49987	nf AL049987	1.47
hardware grants and the second	NH_017999	1.47
opposement principal and the control of the control	969900 HIN	1.47
Pipote cordain	NM_016125	1.43
Conserves includes do ALO21395 ADE = Human DNA secuence from close RP1-269H15 on chromosome 20q12-13.12 Contains a gene similar to popticy/proby isomerase (cyclophilin), part	_	1.47
94 Centrals confidence professe - file		1.4
Consensus includes do 143577 FEL=EST (OB_XREF=gi:899066, IOB_XREF=est:143577 //LONE=EST500 / IOE=Hs. 82171 Homo sepiens (clone 115392) mRNA	143577	1.47
cell division cycle 25¢	NM_001790	4.
RAP1, CTP-CUP desociation stimulator 1	6(001851	
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(CIC4-NOT benearbloon complex, subunit 3	AIRZEASA	9
The modern a chart to the larger comes, 16	X74070	1.67
mark electron latter a	NN_002405	1.47
margar integration of consultant and	NM_005926	1.47
phospholicid transfer protein	NM_006227	1.47
hypothetical protein FLI21799	NM_024946	1.47
purhangi reciptor P27, 6-protein coupled, 11	NN_002566	1.47
smoonphage sprintspylated alemine-rich C kinase substrate	NM_023009	<u> </u>
A-ray repair complementing defective repair in Otinese hamster cells 3	WUC2063	
gloom tumor suppressor anddda'n region gene 2	NW 024073	3
hypothetical protein NELEE75	RC002411	•
forces service seman unung protein i	NM 000144	1.47
The state of the s	AF161454	1.47
Company in the AMONTALE OF Fallows serious (ANK F1109S4 for done PLACE) 000383, highly similar to Home serious mRNA for HTMR1 protein. FEA=mRNA /08_XREF=gi:70.4X001816	0. AX001816	1.47
control breakfairs 2. readility submit 8 (854), ession isotom	NM_006246	1.47
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symptomic Neutrogen interacting protein	NM_004819	÷ :
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Institute of the Control of the Cont	NM 021927	9
The associated, colled-coll containing protein visuse 2	087931	<b>?</b>
phosphotnositide-3-kinase, regulatory subunit, potypopide 1 (p65 alpha)	A680192	1.47
rBonadesse/angiogenin tehbition	NM_002939	1.47
Consenses includes gb-ALD49761 /DEF=Human DNA sequence from done RPS-86307 on chromosome 20p12.3-13. Contains the CSNY2A1 gene for casein kinase 2 alpha 1 polypeptide (EC.		1.47
fath-add-Conzyma A figuse, very long-chain 1	NM_003645	1.47
KF-II mR/N-binding protein 3	KM_006547	9
COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 78	NM_022730	<del>9</del>
DEAD/H (Asp-GL-Na-Nsp/Nis) bos polypspide 11 (CNL1-like helicase homolog, S. cerevisiae)	NM_030653	 9
hypothetical protein DVPZp564D0478	AL136683	9
nuclear transcription factor V, alpha	AL031778	<del>2</del> .
acidation resistance	NM_018002	9
hauf shock 90kD protesn 1, alpha	AF028832	9 9
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LLCI + Gell GANLAGO CYCB 14 Notinging A (2. cerevise)	A-USA1Us M74320	<b>?</b> 4
parameters of the control of the con	NA 014413	£ 4
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imponence protein, one international (mg/script) assured for the contract of nucleolar TGE bank through entering the contract of nucleolar TGE bank through the CMT).	NM 022117	4
Identities A.S. Inceptor	NM 000675	\$
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DW7ZN434F195 protein	BE222901	1.46
ribosomil protein 124	AIS60573	1.46
activ, gamma 1	86026805	<del>.</del>
MAX protein	M64240	46
Onal (Hsp40) homolog, subfamily 8, member 6	AF080569	<del>-</del>
Missillo	NA_018116	\$
eriochendrial ribosomal protein L49	NN_004927	\$
Outsit het, MX240931033100 st Home sapiens CDNA, 3 end /ctone=II/N6E-936607 /ctone_end=3 /gb=MX24093 /gb=2265021 /ug=Hs.23158 /cm=718	M524093	9
hypothetical protein FU22246	MM_025232	ę :
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spectrie, sighs, non-entherecytic 1 (sighs-Indin)	AL110273	1.46
hypothetical protein NGC4172	NM_024308	34.
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NV_01645  AV 11807  AV 11807  AV 11807  AV 11807  AV 105187  AV 1055187  AV 105529	RMA binding protein S1, serine-rich domain	NM_006711	1.37
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enaphase-promoting complex subunit 10	NH_014885	1.35
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	cembid-lipothacinosis, neuronal 2, late infantile (Jansto-Bielschowsky disease)	KM 000391	-
	FAST bines	AX023141	1.31
	hypothetical protein	AA463853	1.31
	similar to hypothetical protein MMC1-2336	86230758	
	U6 snRM-casociated Sm-like protein LSn8	NM 016200	1.31
	Bardel-Bied syndrome 4	AI813772	5
	dhromosome 21 open reuding frame 45	NN 018944	131
	phosphoticy/inoxital transfer protein	H15647	1.3
	SELENOPHOSPHATE STATINETIASE; human selenium donor protein	AI885670	5
	2-5-dispondenylate synthetase 2 (69-71 kD)	NM_002535	13.
	polyments I and transcript release factor	AF312393	1.31
	Interogeneous nuclear ribonucleoprotein AO	NM_006805	1.3
	Action 2	BC003683	131
	Consensus withdess of ALX2226 /F ELXEST /OB_XRES = gi:12785789 / / / / / / / / / / / / / / / / / / /	igur ALS22296	£.
	CONSTRUCTION MANUAL BOOK OF LEASE ST. 708_XREF = 9:6036972 108_XREF = ettab55412.11 //LONE=IMAGE.2560215 /UG=H1.287317 ESTs. Weakly similar to A59252 myosin beeny	y d AW081820	1.3
	An Survey of American	BC000464	<u>.</u>
	Importance protein Local J	MM_017710	<u>.</u>
	with Associated monthly protein 1	NM 002039	<u>-</u>
	Approximate forms 1.10.57	AL 109978	<u>.</u>
	Company ( (mily) and souther ( mily) for some size of som	NM_005186	<u>.</u>
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	IGAN 122 profess	A5226/0	5 5
	филипи	NN 014905	5 5
	hypotherical protein FU22794	NH 022074	5
	transporter 1, ATP-binding cassette, such-family 8 (MOK/TAP)	NM_000593	1.30
	KAMO176 protein	M\$23921	1.30
	VOZ drauž kljurgou-ideli	NM_018200	1.30
	DDM/M (Advantage) and polypeption 28	AC004531	8.1
	INJUDICAL POCHMY PLINCES	NM_018046	2 5
	Investments of process	A600/33C	3.5
	respectively and respectively.	MA_01/83/	2.5
	Forton seasonadoloulous processors and seasonadolous seaso	UM DOOCS	<u> </u>
	(MADA4) one product	8F88244	2 2
	pody (A) binding protein, cytoplasmic 4 (inducible form)	NM_003819	06.1
	department metgel or D2 H13625	H30625	1.30
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remarks and the second of the	NH 027755	1.30
Production forting 1	NM_018209	0.1
Prpothetical protein FU22624	AW043622	1.30
Proodesizal pratain NG MG	AIG81536	8.
cell division cycle 42 (6TP binding protein, 2540)	R37664	1,30
ectivated p21cds 42Hs binase	NM_005781	1.30
Consensus includes go.W652058 /FEA=EST //DB_XREF=g:4736037 //DB_XREF=est:w627411.11 //LONE=IMAGE:2306901 //UG=Hs.129061 Human (hromosome 16 BAC clone (179875K-k-1		1.30
valy-LiNA synthetase 2	8£790854	1.30
hypothetical protein FU10698	AF062733	1.30
golg phosphoprotein 5	AX001574	1.30
crystallin, seta (quinone reductase) site 1	NM_005111	1.30
zinc finger protein 132 (clone pHZ-12)	NM_003433	1.30
Down syndrone critical region gene 5	AB035745	1.30
topocisomerae (DNA) If stoke (1704)	AU159942	1.30
surries (Prescripta) horacio	8E778078	1.30
small nuclear thornthecrotes () polymerside (18k0)	NM_004175	1.30
Consumes includes ab ARO2 2086.1 (DEE = Home susiens CDNA: FLD1 433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 1433 fs. clone (0104232. FEA=mRNA / DB XREF = 01:10437539 (A)G=Hs 306761 Home susiens cDNA: FLD1 143475 (A)G=Hs 306761 Home	FU21433 fis, cs AX025086	1.30
(QAA0176 protein	079998	6.3
misson-echisted protein kinase 1	NM_002745	1.30
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Is braciation elongation tactor, entochondrial	AF110399	1.30
hypothetical protein FU21940	AW975818	8.1
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NS1-associated protein 1	AF037448	1.30
protocologie o	AS24125	1.30
and the second s	NM 003915	1.30
harm merition actions (m96) 1	NN 003299	1.30
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Consequent includes ab AV66 [513 PEA. SET ON XXEE = e1-8/26 [533 KLONE = 61/67 D12 XIGHT = Hx 29/3637 [51].	AV661533	2,3
simal-induced professional cone	NM 006747	1.30
cytochrome c acidese subunit Va	NM 004255	1.30
eakayotic translation laritotion factor 4 gamma, 2	NM 001418	1.30
protein phosphates 2 (hormarks 2A), resolution subunit A (PR 65), beta isoform	179584	1.30
O-linked H-ectylolocosmine (GkVk) transferse (UPP-H-ectylolocosmine polyberbide-H-ectylolocosminy) transferse	AF070560	1.30
IQA0008 own product	NM_014750	1.30
NAD (P.) II defredocentae, cuincre 2	NM_000904	1.30
actin cross-levior factor	AX023406	8.1
Ras-6TPase activating protein SH3 domain-binding protein 2	AB014560	1.30
Omactin 2 (p50)	NH_006400	1.30
Wignettie motificantaining 26	NH_003449	1.30
Sec23-interacting protein p125	AJ332962	1.30
deta-tribuin	85200028	1.30
Rag C protein	NM_022157	1.30
death effector domain-cortaining	AF064605	e
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programmer musice	024183	0.5
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summer consumed recentor expressed in brain 3	NN 018969	1.30
Metch homelog 2 (Oresophia)	AA291203	1.30
decrin	NM_001920	1.30
IDAA0999 protesin	MOHISA	1,30
cholinergic mengtar, nicotinis, alpha polypeptide 7	U62436	1.30
6 protein-binding protein (RF6	NM_012341	1.30
(GI-O5 protein	NM_016408	1.30
(GL-05 protein Canamas includes do XCO24490 (DEF = Koma supiens champsome 13, cosmid R29381 /FEJ=CDS (DB XREF=#2995576 /ME=Hs, 156015 Homo supiens champsome 19, cosmid R29381 /KCO24490	NM_016408	¥

	27,000 100	•
endocine regulator	NA_014343	3 5
superacide dismutase 2, mitochondrial	146368	
dric finger protein 3544	KW_005649	R: :
IDAA0561 protein	A8011133	<b>2</b> 7
Consuments includes db.?15724 (DEF = Home supiens SERCA3 gene, exons 1-7 (and joined COS) /FEA=mRNA /DB_XREF=gi:3021395 /UG=Hs.5541 ATPase, Ca++ transporting, ubiquitous	Y15724	1.29
protein phosphatas 4, regulatory subunit 1	NM_005134	67,1
DAAM Forefrin	AF112221	<u>ي</u>
When derived the second	AL138831	62.1
one would make the second of the second control of the second cont	AL523904	1.29
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metryl-Cpc backing domain protein 4	1100,000	67.
phosphonosticas 3-timese, cetta polypeptice	1000000	9 5
hypothetical protein FU22637	NM_025165	Q :
paratymosin	M24398	1.29
vinentin	M922389	67.1
caterioulin	A348935	57.1
ATTMA. H+ transporting, historicular proton pump), beta potypeptide, 56/58kD, isoform 1 (Ranal tubutar acidosis with deathers)	NM_001692	1.29
Historia Di Domoton I Oresconila	080030	1.29
news seeked from Old with a complete creditor secuence	NM_014628	62.1
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er i i urand gruppou	4004381	2 5
SA (rist hypertexson-associated) homolog	M. 004003	2 2
spiking factor (KCL.3)	מעריים בייני	9
KCI domistram signaling 1	MM_012108	67.
lymphocyte adaptor protein	NA 0054/5	67.
kayapherin (importsi) beta 1	138951	1.29
homolog of vest ribosomes is regulatory protein RRS1	6001811	1.29
Proof action F120166	NM_017702	1.29
borntheir an artist MEC 4126	A357539	62'1
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KIM bridging moot, target standed interacting protein I	00000 NA	<u> </u>
hypotherial protein UN-420-401 664		2 5
Consensus includes gb.M. 197398.1 / DEF EMOIND SEQUENT MENN, CUNA DIV. 264-34A/D2.2 (From clone UIV. 264-34A/D2.) / FEX-EMANA / UB., ANKET = gr.08U/1944 / UU.=HS., 1050.39 FROM SAPRENS FROM	AC13/396	67.
plakophin 4	65526299	67.
Dna (Hsp40) homolog, subtarnity 8, member 9	MM_D12528	57.
hypothetical protein FLZ1736	NM_024922	1.29
BUB3 budding uninhibited by benzimidazoles 3 homolog (yesst)	NM_004725	62.1
Consensus includes gb:XW293356 FEA=EST /OB_XREF=g; 6699992 /OB_XREF=est:UI-H-BI2-ahl-c-11-0-UI-s1 //LONE=IMAGE:2727165 /UG=Hs.58220 Homo sapiens cDNA-FU23005 fis, AW293356	AW293356	1.29
Consensus includes gb.M.255545 / DEF = Homo supiens charmosome 17, HC90, HC71AC, HC6 and HC56 genes, complete sequence / FEA=CD5 / DB_XREF = gi: 10945429 / NG=Hs. 19614 genin	. AF258545	1.29
Winn's tumour 1-associating protein	NH_004906	62'1
guerine nucleatide binding pratein (6 pratein (6 pratein), alpha z polypoptide	MM_002073	67.1
BK(A1 associated protein	ALO42733	62:1
Nerradonin reductase	NM_004110	1.29
MADS bas transcription enhancer factor 2, polypoptide ( (myocyte enhancer factor 20)	N22468	1.29
IQUAD682 gene product	NA_016196	1.29
Obrasics	NM_006708	1.29
RADS! homolog (Reck homolog, E. celi) [S. cerevisie)	MM_002875	67'1
chromosome 6 open reading frame 34	NM_014320	1.29
MCK adaption protein 1	NM_006153	1.29
clathrin, light polypeptide (Lcb)	80006332	1.29
Obcoprotein Y (statelet)	NM_004488	1.29
Procherical protein FU20154	AK000161	1.29
Consensus includes po.XW449390 /FEA=EST /08_XREF = qi:6990166 /08_XREF = est:UI-H-BI3-ab-q-10-0-UI s1 /CLONE=IHAGE:2734650 /UG=Hs.257150 ESTs, Moderalely similar to SUR1,		1.29
DIG7295440092 protein		£7:
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rae-Bla protein	KM_012249	1.29
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OXS cell division cycle Silike (S. pombe)	KH 001253	
forces and aim 16 (103 4)	With Angelos	
the first of the control of the cont	BCCOOL INCOME	
India transcendential relationary syndrotic Artificial (In/U.54 homolog), 2. cerevisite?	028600	
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hypothetical protein FU20125	NM_017676	
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	NH_003992	
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UDP-GalthetaGkNkc beta 1,4- galactosyttmasferase, pohypeptide 5	BF691447	
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hypothetical protein FU22679	NM_017698	
EDP desociation inhibition 1	NM 001493	
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MA_013993	
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habharetic peptide precursor A	M30262	
algor functional domain (FTPRF interacting)	AF091395	
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Consomates included gb-AV733266 /FEA=EST /08_XREF=gi:10850811 /08_XREF=est:AV733266 /CLONE=cdAdJG04 /16=Hs.76325 step    spicing factor SLU7	AV733266	
anhydrae #	M36532	
consensus includes ab:86429214 FEA=EST 708, XREF = ai:13335720,708, XREF = est:602498083F1 KLOME=HMGE+4611836 AUG = Hs. 258144 zinc financ contein 330 (KOX 31)	86429214	
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ementary will construct in protein totals unlass to beta	AA181179	1.28
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e-centri tysp-evanta-rapints) aas parjoepade 9 (ann heintase A, nuclear DNA heintase II; feutophysin) Itaan I BC nevation	BF313B32	1.28
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TO THE PARTY OF TH	NW 000983	1.28
O MARINE SAME AND	297630	1.28
a bookers take	A1081107	1.28
17 manal asker war	NM_006526	1.28
VENERAL PRODUCTS GOIS UNASKY. I VIET = Home saperis, clone IPIAGE: 3629896, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IPIAGE:3629896) //08_XREF = gi:13279244 / BCD04327	XREF = 9:13279244 A 8C004327	1.28
The second section is a second section of the second section of the second section sec	NM_D04368	1.28
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RMA member 21% corrected family	NN_006463	1.28
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FIGOS binding protein 1A (1220)	DIAN FLICUIS IIS, CION ANDOLIAS	1.28
Apha-activin-2-asociated LM pretein	(A) (COO) (A)	9 .
hypothetical protein	AEROTORE	97.
hypothetical protein FU11767	2000 KK	37.
UCAUTH (Job-Abi-Abi-Asp/His) bux polypeptide 11 (CHL1-tike helicase homolog, S. cerenisiae)	A983033	1.28
North Agin Commission (1920)	AA206161	1.28
CMA(A) recording to recording to the control of the	A823896	1.28
Propúblicia profinin FLZ 865	A8030710	1.28
breat carcer anti-estopen resistance 3	NM_022759	1.28
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calcium channel, vottage-dependent, I. type, alpha 10 subuni	KR_000/75	97.1
hypothetical protein FU14827	MF964197	97:1
Nation stimulating homone receptor	M95489	27.
and of profession i	AX024840	1 28
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Specimen prices (100)	AW294587	1.28
major insucuorispatas, tass t, 1 (pseudogene) Estrementaria altra i firmantia altra (t)	M80469	1.28
55 Up mitted states exceeding the control of the co	BC002374	1.28
interfero canima receder	NM_014771	1.28
secreted frizzled-related protein 1	NM_000416	1.28
ribosonal protein 1.26	/0525A /1535631	27.
TP53 larget game 1	A.12.18/1	97.
seven transmentane protein TNISE3	EC/2003G	1.28
deemage stimulation factor, 3' pre-RNA, subunit 2, 64LD	SCELOU MN	87.
hypothetical protein FU12879	-	2 .
Consensus includes abiA972416 /FEA=EST // REFE ai: 5769137 // REFE == 1000000000 AIC 10000000 AIC 1000000000 AIC 10000000000000000000000000000000000		

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Consensus includes gb.AR4.22.736. FUAREST (NB_MILT) = g1.595.53.7.6 (NB_MILT) = est. (NB_MI	86152979	
ribanomal profesin L22	AL080065	
D672/564102 protein	NM 002221	
monitol 1,4,5-trisphosphate 3-timase B	RC000192	
dhydrotolata reductase	25,01134	
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UM0500 protein	NN 006447	
shquitin specific protease 16	7613133	
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INTERPORTING TALKA STRUCKING	NN 024319	
Approchedical protein MC4174	AX021672	
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1672/9868/1523 protein	0000000	
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processing from the selection by selection of the control of the selection member 8	NM_004858	
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478 AB_X8EF=ett*wa05e06.st KLONE=IMAE:2297218 /V6=Hs.81360 Homo sapiens CDV& FUZ1927 fs, clone HEPO41; yndrome) FUZ1499 fs, clone COLO5634. FEA=mbNA, AB_X8EF=g;10437612 /V6=Hs.306373 Homo sapiens CDVA: FUZ1499 fs, ch. pase hase  18630 /AB_X8EF=ett*p068605.st /KLONE=IMAE:3644888 /V6=Hs.296338 ESTs  N N N N N N N N N N N N N N N N N N N
478 708_08EF = est:wa05x06.x1 /KLONE=IMAGE:2297218 /NG=Hs, 81360 Homo supiens cDNv. FU21927 fs, clone HEPO41; yndrown) FLI21 499 fs, clone COLOS634. /FEA=mRNA. /DB_08EF=gi:10437612 /NG=Hs, 306773 Homo supiens cDNv. FU21499 fs, chance complex (COLOS634. /FEA=mRNA. /DB_08EF=gi:10437612 /NG=Hs, 306773 Homo supiens cDNv. FU21499 fs, chance complex (COLOS634. /FEA=mRNA. /DB_08EF=gi:10437612 /NG=Hs, 296338 EST;  BROWN R. K. etylkate complex (COLOS634. / /KLOHE=IMAGE:3644288 /NG=Hs, 296338 EST;  N. N
478 // DB_JREF=extrwaOScO6.11 /CLONE=IMAE2237218 // DE=Hs. 81360 Homo sapiens cDNv. FUZ1927 fs., clone HEPO41; yndrome) F122 1499 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 306773 Homo sapiens cDNv. FUZ1499 fs., c.) F124 1499 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 306338 EST) F126 1499 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F127 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F127 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F127 1499 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F127 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F138 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F139 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F139 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F149 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. /FEA=mRNA./DB_JREF=gi:10437612 // UG=Hs. 206338 EST) F150 1496 fs., clone (CLOS634. // UC=Hs. 206338
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478 /DB_XREF=estwa0Sc06.s1 /CLONE=IMAGE:2237218 /UG=Hs.81360 Homo sapiens cDNX-FUZ1327 fs, clone HEPOM1; yndrome] FUZ1499 fs, clone COLOS634. /FEA=mRNA /DB_XREF=gi:10437612 /UG=Hs.306773 Homo sapiens cDNX-FUZ1499 fs, ch. nase 18630 /DB_XREF=est:7p06b05.s1 /CLONE=IMAGE:3644888 /UG=Hs.296338 ESTs Ne excrytase comples) 1-2
478 / DB_LREF=ext-wa0SeO6.st //LONE= MAGE.2297218 / JUG=Hs. 81360 Homo sapiens cDNA; FUZ1927 fs, clone HEPOA1; yndrowne) FUZ1999 fs, clone (OLOS634, /FEA=mRNA / DB_LREF=gi:10417612 / JUG=Hs.306773 Homo sapiens cDNA; FUZ1499 fs, c4-Jase Anse 18630 / DB_LREF=ext-7poGaO5.st //LONE= MAGE.364488 / JUG=Hs.296338 EST; Anse Anse exctytase complex)  PR H H H H H H H H H H H H H H H H H H H
478 / DB_JXEFE=eti*wa0Sc06_x11 /KLONE=IMAGE:2237218 / J0G=H3, 81360 Homo sapiens cDNA; FUZ1327 fs, done HEPO41; yndrome) FUZ1499 fs, clone COL05634. /FEA=mRNA / DB_JXREFE=g:10437612 / J0G=Hs, 306773 Homo sapiens cDNA; FUZ1499 fs, chase FUZ1499 fs, chone COL05634. /FEA=mRNA / DB_JXREFE=g:10437612 / J0G=Hs, 306773 Homo sapiens cDNA; FUZ1499 fs, chase FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. /FEA=mRNA / J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05634. // J0G=Hs, 296338 FSTs FUZ1499 fs, chone COL05644. // J0G=Hs, chone COL05644. // J0G=Hs, chone COL05644. // J0G=Hs, chone COL05644. // J0G=Hs, chone COL056
478 /DB_XREF=est:wa05c06_a1 /KLONE=IMAGE:2237218 /UG=Hs_81360 Homo sapiens cDNX_FUZ1927 fs, clone HEPO41; yndrome) FUZ1499 fs, clone COL05634. /FEA=mRNA /DB_XREF=gs:10437612 /UG=Hs_306773 Homo sapiens cDNX_FUZ1499 fs, c4- hase H8530 /DB_XREF=est:7p06b05_a1 /KLONE=IMAGE:3644888 /UG=Hs_296338 ESTs H8 excrytase complex) -2
478 / DB_LAEF=ext-wa0SeO6.st //LONE=IMAGE.2297218 / JUG=Hs. 81360 Homo sapiens cDNA; FUZ1927 fs, clone HEPOA1; yndrowe) FUZ1999 fs, clone COLOS634. /FEA=mRNA / DB_LAEF=gi:10437612 / JuG=Hs.306773 Homo sapiens cDNA; FUZ1499 fs, c4-Jase A Hasso / DB_LAEF=ext-7poGaO5.st //LONE=IMAGE:364488 / JuG=Hs.296338 EST; Basso / DB_LAEF=ext-7poGaO5.st //LONE=IMAGE:364488 / JuG=Hs.296338 EST; B HA
778 / 70B _XREF=est:wa05c06.x1 /KLONE=IMAGE:2237218 / 10G=Hs. 81360 Homo sapiens cDNA; FUZ1439 fs., clone HEPO41; yndrome) FLU21499 fs., clone COL05634. /FEA=mBNA / DB_XREF=g:10437612 / 10G=Hs. 306773 Homo sapiens cDNA; FUZ1499 fs., chase Anste 18530 / DB_XREF=est:7p06b05.x1 / KLONE=IMAGE:3644888 / 10G=Hs. 296338 ESTs  N N N N N N N N N N N N N N N N N N N
478 /DB_XREF=estivadSco6_x1 /KLONE=IMAGE:2297218 /UG=Hs, 81360 Homo sapiens cDNA; FUZ1927 fs, clone HEPOA1; yndrome) FUZ1499 fs, clone (COLOS634, /FEA=mRNA /DB_XREF=g:10437612 /UG=Hs, 306773 Homo sapiens cDNA; FUZ1499 fs, chase 18630 /DB_XREF=est:7po6b05_x1 /KLONE=IMAGE:3644888 /UG=Hs, 296338 ESTs  Ne exctylase complex) -2
178 (NB_AREF=estradO&O6.st /(LONE=INAGE.2297218 /NG=Hs. 81360 Homo supiens cDNk FU21927 fs., clone HEPOd1; yndrome) FU21499 fs., clone (OLOS634, FEA=mRNA, NB_AREF=gr:10437612 /NG=Hs.306773 Homo supiens cDNk FU21499 fs., chase nase 18630 /NB_AREF=est:7p06405.st /(LONE=IMAGE.3644888 /NG=Hs.296338 ESTs)
718 / DB_XREF=extrava0Sc06.x1 /(LONE=INAGE:2237218 / J0G=H3, 81360 Homo sapiens cDNA; FUZ1439 fs, clone HEPO41; yndrame) FUZ1499 fs, clone (OLOS634, /FEA=mRNA, / DB_XREF=g:10437612 / J0G=Hs, 306773 Homo sapiens cDNA; FUZ1499 fs, chase fuses  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18630 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:3644888 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=Ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=Ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XREF=Ext; 706805.x1 /(LONE=INAGE:364488 / J0G=Hs, 296338 ESTs  18640 / DB_XR
478 /DB_UREF=estivaOSco6.st /CLONE=IMAGE.2297218 /UG=Hs.81360 Homo sapiens cDNA: FUZ1927 fs, done HEPOAT; yndrome) FUZ1499 fs, clone COLOS634. /FEA=mRNA /DB_UREF=gi:10437612 /UG=Hs.306773 Homo sapiens cDNA: FUZ1499 fs, chase nase ne *cetylase comples) -2
178 / 70b_18EF=est:wa0SeOS.11 //LONE=INAGE:2297218 /JJG=Hs.81360 Homo sapiens cDN.c. FU21927 fs, clone HEPO41; FLIZ1499 fs, clone (CQLOS634, FEA=mRNA, DB_18EF=g;10437612 /JJG=Hs.306773 Homo sapiens cDN.c. FU21499 fs, chase 18630 / 70b_18EF=est:7pO6bOS.11 //LONE=INAGE:3644888 /JJG=Hs.296338 ESTs 18630 / 70b_18EF=est:7pO6bOS.11 //LONE=INAGE:3644888 /JJG=Hs.296338 ESTs 18630 / 70b_18EF=est:7pO6bOS.11 //LONE=INAGE:3644888 /JJG=Hs.296338 ESTs
478 ADB_AREF=extr=a0Se06.st /KLONE=IMAGE.2297218 /NG=Hs.81360 Homo sapiens cDNx FUZ1927 fs, clone HEPO41; yindrome) fill21499 fs, clone COLOS634. /FEA=mRNA /DB_AREF=gi:10437612 /NG=Hs.306773 Homo sapiens cDNx FUZ1499 fs, clone COLOS634. /FEA=mRNA /DB_AREF=gi:10437612 /NG=Hs.306773 Homo sapiens cDNx FUZ1499 fs, close COLOS634. /FEA=mRNA /DB_AREF=gi:10437612 /NG=Hs.306773 Homo sapiens cDNx FUZ1499 fs, close COLOS634. /FEA=mRNA /DB_AREF=gi:10437612 /NG=Hs.306773 Homo sapiens cDNx FUZ1499 fs, close COLOS634. /FEA=mRNA /DB_AREF=gi:10437612 /NG=Hs.206338 ESTs ne **etylase complex)
478 / DB_XREF=ett-wal05c06.st //LONE=IMAGE.2297218 / VIC=Hs. 81360 Homo sapiens cDNA: FUZ1927 fs, clone HEPO41; yndrome) F122 499 fs, clone (CLOS634, /FEA=mRNA / DB_XREF=gi:10437612 / VIC=Hs. 306773 Homo sapiens cDNA: FUZ1499 fs, chase f122 499 fs, chone (CLOS634, /FEA=mRNA / DB_XREF=gi:10437612 / VIC=Hs. 296338 ESTs l8630 / DB_XREF=ret:7p06b05.st //LONE=IMAGE:3644888 / VIC=Hs. 296338 ESTs ne *cetylase comples) 1.2
8 MB_18EF=est:wa0\$c06.st / KLONE=IMAGE.2297218 /Ji6=Hb.81360 Hamo sapiens cDNV: FUZ1927 fs, clane HEPO41; 22 days fs, clane (CUOS634, /FEA=mRNA /MB_JREF=gi:10437612 /Ji6=Hb.306773 Hamo sapiens cDNV: FUZ1499 fs, chose (CUOS634, /FEA=mRNA /MB_JREF=gi:10437612 /Ji6=Hb.306773 Hamo sapiens cDNV: FUZ1499 fs, chose (COMPA)
743 /09_AREF=ext;va05e06.st / KLONE=IMAGE.2297218 /UG=Hs, 81360 Homo sapiens cDNA; FUZ1927 fs, clone HEPO41; yndrome) FL121 499 fs, clone COL05634. /FEA=m&NA /DB_AREF=gi:10437612 /MG=Hs,306773 Homo sapiens cDNA; FUZ1499 fs, clone COL05634. /FEA=m&NA /DB_AREF=gi:10437612 /MG=Hs,306773 Homo sapiens cDNA; FUZ1499 fs, clone COL05634. /FEA=m&NA /DB_AREF=gi:10437612 /MG=Hs,296338 E515  ne *Ketylase complet)  2.2
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	R10150	1.18
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IDANO164 game product	KM_014739	1.18
hypothetical protein R30953_1	AA431984	1.18
hypothetical protein FLI20804	NH_017960	1.18
Conservus includes ab A 35954 (DEE a furman DNA sequence from clone RP 11-318P23 on chromosome 20 Contains a TAR DNA-binding protein pseudogene, ESTs, STSs and GSSs /FEA=ET	1, STSs and GSSs /FEA=CT AL359954	1.18
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Consensus includes gb.28351 /DEF=Human DNA sequence from PAC 56089 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 605 nibosomal protein L4 pseudogene RNA binx 298751	L4 pseudogene RNA binc 298751	1.17
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cold shock domain protein A	ALS56190	<del>-</del>
integral membrane protein 28	AF092128	-
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MY_01871 NY_01873 NY_01874 NY_01873 NY_01874 NY_	NM_006207	1.14
MM, 018179  MM, 018170  MM, 01	NM_015711	¥.
MO22566  MO22566  MO22566  MO22566  MO22566  MO22566  MO22566  MO22566  MO2256  MO2256  MO2256  MO2256  MO225738  MO20576  MO20579  MO20579  MO20579  MO20579  MO20579  MO20579  MO20579  MO20570  MO2057	NH_018179	<u>.</u>
## AM022566 547238  ## C03982  ## C03839  ## C03830  ## C03831  ## C03832  ## C03832  ## C03832  ## C03832  ## C03831  ## C03832  ##	AK026910	<u>:</u>
1443 / CLONE = INAGE.2813610 / MG=Hs. 132299 ESTs	AX022566	<u>*</u>
MM_018563  NM_018563  NM_0185640  NM_0185640  NM_018164  NM_018164  NM_018164  NM_018164  NM_018164  NM_018166	567238	<b>Ξ</b>
MC00450  MC0450  MC0144  MC0314  MC0144  MC0144  MC0144  MC0144  MC0145  MC0164  MC01780  MC0164  MC01780  MC005174  MC005177  MC005177  MC005174  MC005177  MC00517	NH_003982	<u>*</u> :
NH, 004501 NH, 002379 NH, 002370 NH, 003370	KM_U18563	<u>*</u> :
HIL-002391 HIL-002391 HIL-002391 HIL-002391 HIL-002391 HIL-002391 HIL-002391 HIL-002391 HIL-002311 HIL-002311 HIL-002311 HIL-002312 HIL-002313	AR3034/6	•
AM13351  1:6009447741 ALONE = IMAGE: 2960610 Aug = Hs. 106843 Ann = 765  AM13351  1:6009447741 ALONE = IMAGE: 2960610 Aug = Hs. 218329 hypothetical protein Atl = gb: NH_015383 1 IEC299495  8:101048  A033143  8:101048  A033143  8:101048  A033143  RM_03350  RM_033163  RM_031439  RM_131516  RM_131616  RM_13161		
Wi193511  Wi19351  Wi193511  Wi19351  Wi193511  Wi19351		=
16009447741 / CLONE=HMAE.2960610 / Jul=Hb. 218329 hypothetical protein /FL=gb.HM_015383.1 RE29495  8 F11523  8 F116323  8 F1	_	<u> </u>
# # 19223   KOO1046   MOS145   MOS154   MOS155	_	7
### A FILL   18040 FLU   18040	BF115223	÷:
31:JUI 1480-40 /LLONE=MAMMALOOZ-428 /MG=Hs, 301615 Homo sapiens cDNA FLIZ370 fs, done MAMM ALIAGO-40  NH	BC001048	¥.
NH_00350 NH_0032123 NH_004295 NH_004295 NH_004295 NH_004295 NH_004296 NH_004		<b>Z</b>
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HY_018126 HY_002477 HY_002477 HY_002477 HY_002477 HY_002595 HY_002595 HY_0025174 HY_005174 HY_005174 HY_005174 HY_005174 HY_005174 HY_005174 HY_005174 HY_005175 HY_00455 HY_00455 HY_00455 HY_00455 HY_00455 HY_00455 HY_00455 HY_005173 HY	NM 022128	
NH_004277  NH_006296  NH_006296  NH_006296  NH_006296  NH_006104  NH_006104  NH_006104  NH_006104  NH_006104  NH_0061064  NH_0	NM 018126	· -
NN, 006296  AN27744  NN, 077070  NN, 077070  NN, 077071  NN, 077119  NN, 07711	NM_024777	1.1
M7277 444  M7277 444  M7005174  M7005174  M7005174  M7005174  M7005171  M700517  M700617  M70	NN_006296	7.1
NH_017870  RM_0055174  NH_006184  BF221832  NH_006511  NH_006511  NH_00455  NH_00455  NH_00455  NH_00455  NH_00455  NH_00455  NH_00455  NH_00213  NH_00213  NH_00213  NH_00213  NH_00213  NH_00213  NH_00213  NH_00213  NH_00313	AW237404	1.14
## 006184  ## 006184  ## 006184  ## 006184  ## 006184  ## 006184  ## 006181  ## 006181  ## 006181  ## 006182  ## 006183	NM_017870	7.
MT. COOS 184  MT	BC005174	7
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HI_Q20661 A771219 A771219 A771219 MI_Q00380 MI_Q00380 MI_Q00455 MI_Q00455 MI_Q00455 MI_Q00451 MI_Q00451 MI_Q00451 MI_Q00451 MI_Q01213 MI	115000 RN	1.
M771219 M77121	NN 020661	7.
NM_000380  DNZ 2564N1963_s1 /CLONE = DNZ 2564N1963 /NG = 15,22370 Homo supiens millivit. cDNA DNZ 25640 AL038640  NM_00455  AF25579.2  NM_00455  NM_003227  NM_003227  NM_003237  NM_003380	A721219	=
UV 429504N1963_S1 / ALUNE = DV4 429564N1963 / AC = 115, 22370 from suprens mithe, cDNA DV67p5640 AC 356540 AC 356540 AC 3565792 AC 355792 AC 35579	NM_000380	1.14
MA_COMESS  AFESSIVE  AFESS	s mRNA; cONA DKFZp5640 AL036840	<b>*</b>
M. C001004  M. C00	NM_004855 45355703	<b>:</b> :
NA_000491 NA_005227 NA_005335 NA_005335 NA_005335 NA_005237 NA_005337 NA_005337 NA_005335 NA_005337 NA_00537 NA_	87001004	? :
HM_003227 HM_005535 HM_005535 HM_012113 HM_012113 L25541 HM_012418 HM_012418 HM_005515 HM_0055236	NM 000491	3 5
NP_005335  NP_001213  NP_001213  NP_001213  NP_001213  PP_005050  RP_005050	NH 003227	1.13
H. (212) H.	NM_005535	13
	NM_021213	1.13
NY_C1248  AUIST515  AUIST515  AUIST515  AUIST516  AUIST516  AUIST516  AUIST516  AUIST516  AUIST516	17571	1.13
10,2515 10,2510 10,25136 10,25136 10,25136 10,25137 10,25	NM_012418	1.1
ALX4354 81926436 8195603	AUI5/515	E : :
80956148	ALL049547	3 :
THE AMERICAN	96+27730 96+27730	3 5
	W37846	=
	X	MAY 01532  MAY 01533  MAY 01533

Histore that brotein 14, pregramsy-associated endometrial alpha-2-globulin, alpha uterine protein)  gin (placental protein 14, pregramsy-associated endometrial alpha-2-globulin, alpha uterine protein)  groupside N-acetylgalactosaminyttransferase 7 (GalVAc-T7)  propride N-acetylgalactosaminyttransferase 7 (GalVAc-T7)  Trobein 1  1  1  1  1  1  1  1  1  1  1  1  1	NH_004579 NH_001413 NH_001413 NH_001306 NH_001306 NH_001306 NH_0016309 NH_001400 NH_001400 NH_001400 NH_001400 NH_001400 NH_001400 NH_001400 NH_001301 NH_001301 NH_001310 NH_001310 NH_001310 NH_0013110	<u> </u>
faminyl cyclaes]  gen (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)  og sporters), member 2  sporters), member 2  sporters), member 3  schola sporters (fall-Wr. 17)  schola sporters clone 23551 mRNA sequence. If EA=mRNA /DB_JREF=gi-2652606 /JC=Hb. 184019 Homo supiens clone 23551 mRNA sequence  sportein 1  1  1  1  1  1  1  1  1  1  1  1  1		555555555555555555555555555555555555555
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tein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)  og  sporters), member 2  sporters), member 2  sporters (GallAk-77)  prepride N-acetylgalactosaminytransterase 7 (GallAk-77)  stroken sapiens clone 23551 mRNA sequence. FEA=mRNA /DB_JREF=gj:2852606 /UG=Hs, 184019 Homo sapiens clone 23551 mRNA sequence  protein 1  1  1  1  1  1  1  1  1  1  1  1  1		898888888888888888888888888888888888888
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sporters), member ?  sporters I (Gall Mc-T7)		: <u>222222222222222222222222222222222222</u>
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Speptide N. Lechygalactosaminyttransterase 7 (GaNVA-17)  Tereting		999999999999999999
ppopide N. acetygalactosaminyltransferase ? (GalNkc-T7) = Probeide N. acetygalactosaminyltransferase ? (GalNkc-T7) = Probeid 1    Cosamine (UDP-dicNkc) transporter), member 3		: 2
racting = Thomas supiens clore 23551 mRNA sequence. /F.E.A.=mRNA /D.B/JREF=gi-2852606 /J.C=Hs. 184019 Homo supiens clore 23551 mRNA sequence   protein 1		333333333333333333333333
entaing  =Thoma supiers clore 23551 mRNA sequence. FEA=mRNA /DB_JREF=gi:2852606 /UG=H3, 184019 Homo supiers clore 23551 mRNA sequence  protein 1  1  1  1 (The lamity, small GTP binding protein Rac2)  Ypepside  2504		: <u> </u>
rencting Tethons supiers clone 23551 mRNA sequence. If EA=mRNA DB_JREF=g/2852606 AUC=H3.184019 Homo supiers clone 23551 mRNA sequence protein 1  Coamine (UDP-G(cNAc) Transporter), member 3  ( fore lamity, small GTP brinding protein Rac2)  Ypeptide  2504		: 3
=Homo supiens clone 23551 mRNU sequence. If EA=mRNU /DB_JQEEF=gi:2852666 /NG=Hs.184019 Homo supiens clone 23551 mRNU sequences problem 1  1  1 (The Lamity, small GTP binding protein Rac2)  1 (Protection).		: 3
protein 1  1  1  1 (The larrity, small GTP binding protein Rac2)  Ypespiide		355555555555555555555555555555555555555
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1 Cobamine (UDP-GLOMK) transporter), member 3 (The lamity, small GTP binding protein Rac2) Ypepride	MM_002279 NM_002279 NC00467 AC003660 AC0036617 AC1246641 AC124641 AC1246	399999999999999999
coamine (UDP-GicWc) transporter), member 3 (for lamity, small GTP binding protein Rac2) (typeptide	MT-002872 MC005467 MC028667 MC028687 MC02818 MC00319 MC00319 MC00319 MC00319 MC00319 MC00319 MC00319 MC00319	3888888888888888
Cotamine (UDP dicNex) transporter), member 3 ( the lamity, small GTP binding protein Rac2) //peptide	0,000-000 1,002.837 1,002.845 1,002.845 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314 1,002.314	399999999999999
Sociamine (UDP-GictMc) transporter), member 3 ( (no family, small GTP binding protein Rac2) hypopide	N. 19266J M. 15329 N. 1526617 N. 1566617 N. 1526617 N. 1526513 N. 1526513 N. 1526513 N. 1526513 N. 1526513 N. 1526513 N. 1526513 N. 1526513	3999999999999
cosamine (UDP-GicNAc) transporter), member 3  (for lamity, small GTP binding protein Rac2)  typeptide	N. 1528, H. 15329 H. 1586617 A. 7266617 A. 7266617 A. 726641 A. 72	3939393939999
Cosamine (UDP dicNe) transporter), member 3 (Ino lamity, small GTP binding protein Rac2) Speptide	H15323 WZ26617 AZ46641 AY72858 NH_003319 NM_003334 NM_01763 NG05136 MX45954	399999999999
cosamine (UDP-dicNAc) transporter), member 3 ( (no family, small GTP binding protein Rac2) hypopiide	M246611 A724661 NN_003319 A602334 A602334 KC05136 NK_005136 A734954	39999999999
cosamine (UDP-GicNAc) transporter), member 3 (for lamity, small GTP binding protein Rac2) (tho lamity, small GTP binding protein Rac2) (typeptide	NZ50541 NY, 003319 AB002374 NH, 01763 BC005136 NA745954	
cosamine (UDP dicNAc) transporter), member 3 (Ino lamity, small GTP binding protein Rac2) Speptide	MY 203319 NH_003319 AB002374 NH_01763 BC002376 NH_002872	
is (the family, small GTP binding protein Rac2) ypespilde	Nn_003319 A8002374 NN_017563 BC005136 NH_002872 AA745954	
cosamine (UDP-GitMs) transporter), member 3 (fine famity, small GTP binding protein Rac2) typeptide 5504	ABOOK 314 NH_017763 BKOOS136 NH_002872 AA745954	
Cobamine (UDP-Sit-Wac) transporter), member 3  (Ino lamity, small GTP binding protein Rac2)  Specialse	MT_U1/763 BC005136 NM_002872 AA745954	355555
(no tamiy, small GTP binding protein Racz) ypeptide	84002136 NH_002872 AA745954	39999
ypeptide 2504	A745954	19999
Ypeptide 2504	2000	3555
ypepide.	NM 017740	5.5
Ypestide 2504	A8033823	1.13
886	ня 000703	
884	A950314	1.13
585	80003693	1.13
5504	NH_014500	1.13
8594	80000704	 
7904	N659957	1.13
3504	NM_005355	=
	NM_024299	E :
	NA_U22035	3
enhancer of zeste homolog 1 (Drosophils)	A-0521/9	? :
Consensus includes gb.MG251911 / DEF Erlone suplens (DNV-FLI21538 fts. clone (DL06151, FELX IRE SERVICE) B 186F = 11 OCT   CONSENSUS INCRESSION SERVICE SERVIC	ABUUC388	7
contactin, apha 1	AW050627	=======================================
econtine I, soluble	KM_002197	1.13
The state of the s	BC005329	1.13
Industrial prices, so sensor, 2010; polypere c	90002363	1.13
in Descriptions of the Control of th	AX021433	<u>.</u>
1,752	A339541	5
	AW02/923	E :
cpide 8"	NN 003092	? :
receptor interacting protein	NM 016290	=======================================
	076549	1.13
	NH_004573	1.13
	NH_004427	9
		1.13
l enkrikpsy mkink tor growth hormone releasing hormone receptor printary spice variant, complete cds. /FEK=mRNA /GEN=GHRHRpsv /PROD=growth }		1.13
designing and the control of the con	NH_003347	1.1
	KM_006554	=

hencedhedic al restricts [12347]	NM 024723	1.13
Shridket growth tactor 22	NM_020637	9
urgorphyrinogen decarbarytase	M14016	=======================================
SUNO-1-sperify professe	KM_015571	Ξ.
ATP-binding cassatta, sub-family ( (CTR/NAP), member 1	NN_004996	1.13
Consensus includes ab. AMSA 3076 FEA=EST (708, XREF = a; 2291556, 708, XREF = est; nPS6/02, s.1 XLOME=14A42, 82.171 Horro sapiens (clone 115392) mRNA	A543076	1.13
manocidase, atha, class 18, member 1	NM_016219	=
protein tyroeine phosphatase-ièle (proline instead of catalytic arginine), member a	NH_014241	=
SW/SHE related, mubit associated, actin dependent regulator of chromatin, subfamily c, member 1	AL040633	
testis expressed sequence 138	KM_031273	=
hypothetical protein 8C002942	AI081535	 5.
hypothetical protein FU14360	N38751	1.13
interleubin 19	NM_013371	<b>2</b> .
hypothetical protein FIL20354	NH_017779	2
homedog of mouse qualiting QPD (IXH domain RNA binding protein)	A114716	=
hypothetical protein MEL2776	NM_025265	<u>-</u> -
C-rays promoter-binding protein	8£268538	1.13
HIV associated factor	NH_006462	= :
homolog of yeart MOG1	NH_014185	= :
chandration suffee protecytican 4 (inclenoms-associated)	BE857703	1.13
Deleted in split-hand/split-frod I region	NK_006304	<u>=</u>
dysform, lind girdle museular dystrophy 28 (autosomal recessive)	NH_003494	<u> </u>
hypothecia protein PU1786	NM_030892	2 :
Importace protein 3 (Aul 11 4/9)	287120 MM	2 :
Alfess, Ma+/At transporting, beta 4 polypeptice	HA_012069	3:
Amotional Adhesion molecule	A-154005	3 3
CONSIDERATE SPANGES 333. 1 (DEF Elformo suprems CDNA EU 13876 fis, clone EH/RO1001401. /FEA=mRNA /DB_XRE=gr:10438033 /UG=Hs.287604 formo suprems cDNA EU 13876 is a Auditory	5 AK023938	3 :
i cell, immune regulator i	KM_006019	= :
CONSOURCE STATES STATES TOB JARF = 9:1324112 /OB JARF = est5024122581 / ALONE = INAGE: 423487 /AG=H3.97459 YI transcription lactor / Li=gp:H77658.1 gt 86390641	t 56390664	<u> </u>
Consensus includes go.Ve.0564331 (DEE Homs success done 1803 Conductual region mRNA, InELizanRNA (DB_LNEE sp.3044131 (UL=16) Broms success done 1803 Conduct Arbobet 3.	c Ar056453	2 :
embarce of hamentation   {das-like dockung; \times socialed substrate related}	UB431/	3 9
Modern 1	NA_00456	2 9
Inducate process to the control of t	NA 019237	2 5
described and appear of the control	RCOASA6	<u> </u>
Pil demonstration 4	W22625	=
(TDO) 5 creation	NX 014040	=
entropin, teta. 2 (destropin-associated protein A1, 5940), basic component 2)	AA741303	9
SWA-70 protein	BC000134	=
haptodochin-retated protein	KM_020995	1.13
endoplasmic motulum duparone SIL1, homolog of yeast	HH_022464	.13
Consums includes gb.AL008730 (DEF = Human DNA sequence from PAC 48717 on chromosome 6421-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, ST AL008730	1 AL008730	
HSYCOA7 protein	NH_014147	==
humarjac alone attac hydrolase (humarjac alone etase)	NM_000137	= :
percusional biogenesis factor 16	AB016531	<u> </u>
And the state of t	MM_004518	2 3
Undergram workers grass 33 y (cr. = numan tive sequence from FAL 30/11) on chromosome Ages, 5-27.3, unitains to 3 mostoma protein Lev. (LA1, L30) like gene, L313, 313 and a pay QIMA transfer protein Lev. (LA1, L30) like gene, L313, 313 and a pay QIMA transfer protein Lands (LA1, L30) like gene, L313, 313 and a pay QIMA transfer protein Lands (LA1, L30) like gene, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L41, L313, 313 and a pay QIMA transfer protein L413, Albanda transfer protein L413,	AX001406	3 5
construit development trates	NH 006324	9
chromone S com marked from 4	H93077	= =====================================
abitC002877.1 (OEE siteme supports. Smilar to hypothetical protein FU11585, clane HGC:11258, mRNA, compare cds. FEA=mRNA, PROB=Similar to hypothetical protein FU11585 (OB.) 8C002877	1 80002877	=
insuliniika growth factor 2 receptor	NM_000876	1.13
IQAA1069 protein	AX022610	1.13
FIGOs binding protein 18 (12.6 kD)	AF322070	1.13
hypothabicial protein FU20069	KM_017651	1.13
interferon, alpha 17	H38289	<b>=</b> :
T. C.	A6035266	27.
A CYSTOMEN AND A CYSTOMEN A CYSTO	U36190 NB 003164	27.
Al A Good promoting profession and an analysis of the Annal	A1913365	7.7
herothetical control (1105E)	NH 018147	2
Impodential protein EU12035	NM_022771	7.1
	A890947	1.12

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	A.536319	71.
MAL, remote IA3 oncogene temsy	W189609	1.12
bow density lipopratein receptor-related pratein 8, apolipopratein e receptor	NM_004631	1.12
Gaphorae (NUR) (criothrone b-5 reductase)	REFOOD MM	1.12
Institute with sec (2 3 sections because and sections)	200000	
Secretary of the secret	7003007	7.
- Second	A8023148	1.12
KQM1039 protein	AX000478	1.12
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mention educated at a former 21 percentation entries 22 state indices and 100 (20) has been	2000 MM	
more stage of the control of the con	81/700~NM	7.1
magnitude mentione protein	NN_014319	1.12
hypothetical protein FU22329	NN 024656	1.12
Fanconi anemia, complementation croup A	NA COOLSE	:
supposes of it a homology of a committee	551000 mm	•
white come of the transmitted of the contract	NA_003168	1.12
R4 modi containing 6 i Pase activiting protein 1	KM_003870	1.12
Consensus includes gb:UL354872, (DEF = Human DNA sequence from clone RP11-42015 on chromosome 1. Contains 515s. 515s. 655s and a Co6 island. Contains the CH one for two inclines	H nene for two isofon Al 354872	-
DEAL HANGE, M. Ann Chill has nathernoide 10		:
Company of the compan	MA_WISS	7.1
formion (A)	AK023421	1.12
protein prospirative methylesterize-1	AL040538	1.12
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Proorthetical contain EL2003.6	COLON MI	! :
	NA_01/632	7.7
propriocesterase by	W73272	21.1
Oystalin, zeta (quinone reductase)	983100 MK	1.52
themisdate symbolise	10000 100	:
2000	200	•
- Company of the Comp	KM_015332	≃:
solute camer tamiy 25 (mitochondrial carrier, brain), member 14	AF155810	1.12
(QAAO17) protein	41400490	:
	OCCUPANT OF THE PROPERTY OF TH	71.
110000000000000000000000000000000000000	NM_016069	2.1
homeo bas 17	NM 004502	1.12
ONG 27 434F 195 pretein	44010477	3
Proofbetod orders EU10008	ototto HA	::
1 April 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0/6/10_	7.
The state of the s	AL117620	~:
PACE POCKET	AY00\$268	1.12
COX11 homalog, cytachrome c axidase assembly pratein (yeast)	80005895	1.12
actin cross-finiting factor	W6:052	2
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Market and the Control of the Contro	A COOK	21.
Colored and an arrangement	C20+20-MN	1.15
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Consumus includes gb.AL023544 (DEF=Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnumi-2) gene for HIV type 1 Enhancer-binding Pros		<u>-</u>
TAMOTS protein	N9\$226	-8
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engathment and cell mobility 2 (ced-12 homolog, c. elegans)	NM_022086	2
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Dayshinin	AF349720	<u>\$</u>
retinoblastoma binding protein ?	KM_002893	<u>8</u>
thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakanyocyte growth and development factor)	032047	<u>e</u>
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Propodiedical protein FU20345	VM_01777	<u>s</u>
signal peptidase complex (1810)	NH_014300	<u>.</u>
hypothetical protein FU21820	NH_021925	8
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congulation factor IJ (plasma thromboplastin antecedent)	NA_000128	5
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ecetyl-Consyme A erytrensferse 2 (mitochondria 3-asoscyl-Consyme A thiolase)	AW072302	<b>E</b>
Chaster Incl. AW014295U14-B1Op-bast-a-07-0-UI.st Home supiens CDN4, 3 and /clone=IMAE-2710573 /clone_end=3 /gb=AW014299 /gi=5863056 /ug=Hs.238968 /len=391	AW014299	8
wichquitin-conjugating ansyme E20 2 (UBC4/5 hamaiag, yeast)	NA_003339	6
(D28 antigan (Ip44)	KM_006139	\$
ref finger protein 2	NM_005798	8
regulatory factor X, 1 (influences HLA class II expression)	NM_002918	1.09
interferon-related developmental regulator 1	AX747426	8
BCL2-Eng 2		.9
go.4277175.1 / DEF = Home sepsions PNAS-138 mRNA, complete cds. / FEA=mRNA / PROD=PNAS-138 / DB_XREF=gi-12751080 / UG=Hs.326790 Home sepsions PNAS-138 mRNA, complete	ะ	8.
BRCA1 associated protein	AF035620	8
Rho GTP ase activating protein 8	NM_015366	8
bone marphogenetic protein 15	NM_005448	8.
Land protein	NM_014463	8:
call division cycle 258	AL 109804	<b>S</b> :
ademylate kinase 1	NK_000476	8:
palmitoy-protein thioesterase 2	AF020544	<u>8</u>
bone marphogenetic pratein 3 (osteogenic)	NM_001201	<u>-</u>
ribonudeze 6 procuror	KM_003730	S :
XIAMON I gave product	A5007871	8.
dual-specificity tyrosine-(1)-phosphorylation regulated kinase 2	109216	8 3
matta metalloprotainuse   4 (membrane-inserted)	X83535	8 8
hypothetical protein NEL2574	NA_004038	5 5
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CONTRACTOR	N29717	9
hardward government in entry to a few mental services to the s	AKD23092	8
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Proportion protein FL20258	80004907	60.7
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nuclear nuclear substantly 2, group F, member 6	A1935343	6.1
Remblast growth factor meetites 4	NM_002011	8:
protein phosphalase 2 (formerly 2A), regulatory subunit 8" (PR 72), alpha isotorm and (PR 130), beta isotorm	AL389975	8.
deherelled, dsh homolog 3 (Drosophila)	049262	6.3
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pro-malarial concentrating hormone	KH_002674	1.08
77 autocuration of page 277	KM_006477	8
Opdonien 2	AKD01029	1.08
ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	BE621259	1.08
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Appropriate Protein Net 42.76 similar to (68)19	86387555	80.
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hypothetical protein FLI10206	NH_018025	8
transcription factor 12 (MTF4, helia-loop-helia transcription factors 4)	ALS59478	1.08
bile acid Comzyme A: amino acid N-acytrzansferzse (głycine N-choloyfuransferzse)	NM_001701	1.08
BCL2/adenovirus E18 1940 interacting protein 2	BC002461	1.08
hypothetical protein FU12567	NM_024714	<b>1</b> .08
immunoglobulin lappa varlable 1-13	_	1.08
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innunopobulin supertamiy, member 4		1.08
Physocretal protein N462550	-	<b>8</b>
New Asylptonic Comments of the		8 9
AUGUSTA SOLUTION 1997 (TCL-21 / 102-AICE - ESTAUL 1/ 0.5) (LUNE HANNALIUU IS IS / 10E-FIX.296/13 flomb sapients CURA FUI (2.29 FIX, 100n FAARM ALI) 4 (8.50 FIX) (10		3 3
reflects from STE state, it is the state and the state of	\$77580.W	8 8
The second section of the second seco		3 8
served/arginine repetitive mutrix		801
neurotensia receptor 2	•	8.
curritine exceptional errase		1.08
Consensus includes go.M323734 /FEA=EST /DB_XREF=g: 5661698 /DB_XREF=est:wo34g08.x1 /KIONE=INAGE:2457278 /UG=Hs.110613 KIAA0220 pratein		1.08
putable Letype neutral arrate acted transporter		8.
Process programmes ( goldatory (inhibitory) subunit 11  (Print and any programmes)	6	8.
erickmenter promonin 255 enhance non-ATD-se 10	A-280034	80.0
MV. I we bringing gradien?		8 8
neural cell achesion molecule )	U63041	8
endoptasmic reticulum azidonaductin 1-libeta		8
6 protein-coupled receptor 44		8
retinoir and receptor, alpha		88
Imperent suffitte (glucosamine) 3-0-sulfotransfersse 381		80.
ralk bindring protein 1	NM_006788	.08
interference regulations factor §		8
control summary latter ( macroprings)	K37435	8

interlucing Streety or	NM_002186	88.
Authorism to content of temporary and tempor	KM_006995	8.
Production protein DIS Limitar to which witherness of his financial	MH_012410	8
Commens includes 40-JU134977 /FEA-EST //8 JVEE = 1:19995516 /// // JVEE = 1:10995516 /// JVEE = 1:10995616 /// JVEE = 1:10996616 /// JVEE = 1:1096616 /// JVEE = 1:10966616 /// JVEE = 1:10966616 /// JVEE = 1:10966616 /// JVEE = 1:10966616 /// JVEE = 1:1	A828531	83
KAM1653 protein	//S/51/1	8 3
Dipartite modi-containing 2	ALT1/323	3
transducer of ERBS2, 1	A#0/1/95	8.
COLIT homotop, estachrome coxidas assembly matein (vess)	W6/5892	8
hypothetical protein FU22167	MM_003694	80.
hypothetical protein FU12707	MARO 1703	80.
solute carrier family 7, (cationic arrino acid transporter, y+ system) member 11		8 8
hypothetical protein PR00899		8 6
0 site of albumin promoter (albumin D-box) binding protein		3 3
hypothetical protein		707
hypothetical protein FU20030		6.0
Calmagin	79/10 HH	6.5
KAX protein	¥	6.
KQA036s protein	1003355	6.5
ditydolipoemide branched chein transacytase (E2 component of branched chain keto acid dehydronensse complex; manie svonn unine diseases		6.0
action A receptor, type 15	•	.00
poly (A) -specific ribonuclease (deadem/stition nuclease)		6.0
Consensus includes go-M205593 /FEA=E31 /08 /XRF = gi-1803601 /08 /XRF = gi-12058-06 st //LIONE=LIMARE-646760 /III = House po-M20593 /FEA=E31 //OB /XRF = gi-12058-06 st //LIONE=LIMARE-646760 /III = House po-M20593 /FEA=E31 //OB /XRF = gi-12058-06 st //LIONE=LIMARE-646760 /III = House po-M2059-06	n e	6.
hypothetial press DETp56400478		1.07
ubiquitin specific protesse \$ (Isopepidase T)		6 5
deosyhypusine synthase		6.5
partial transcript encompassing TH(2) 1630 cene	*	1.07
6 protein-coupled receptor insus-interactor		1.07
H-44 antigan	030	1.07
apoptous inhibitor \$		1.07
Proodbetical protein HC(13.6.)	<b>.</b>	1.07
retinos and represible protein		1.07
Quotier Inc. 1927(8:2)44(c)4   Home serving (INA. 3 and Prince 1946) 204.09 (April 1942) 444-100-100-100-100-100-100-100-100-100-	167	1.07
bristomics creat factor beta-activited bisses-bindion events 1		1.07
major histocomacibility complex. class [1,00 bes.	MM_006116	1.07
Production protein FU1 (633)		1.07
Consensus includes op: W7454 FEATEST OB XREF = #1 134781 OB XREF = #1 147810 of AT ONE THANKS ALEGGY AND ALL ASSAULT.		1.07
Consensus includes go.AW979196 FELECST (DB. XIEE =q:3170464 // DB. XIEE =q:157193106 AIL = H. 202713 FCT in Advanced in the contract of the co		1.07
hypothetical protein FU23393		6
thrucksookide repeat containing 11 (TMR-essociated protein, 230 kDs subunit)	MA_UC4639	9.5
redear protein, state-telengiectasia locus		) i
V-eta en/throblastosis virus E26 oncogene homolog 1 (avian)		.07
potossiem channel, subfamily K, member 10 (TREK-2)		70.7
iemunoglobulin kappa constant	=	70.1
HDCMA18' protein		7.07
hypothetical protein FU11467		6.6
hypothetical protein FLI20123	2 3	6.6
Consensus includes \$6,4109705.1.0EF = Home supiens mRNA full length insert cDNA clone EUROHAGE 73337. FEB.=mRNA /DB X8EF = ai 56,89834 /ME=H+ 9997 Home surions mRNA & air 10,80705		6.0
dondritin suffite proteogycan 6 (bankan)		9 6
hypothetical protein PR02325		6 6
hypotherical protein FU20596		107
hypotal-inductive protein 2	2	701
hopern witte 2-0-sufformsferse		6 6
MV-1 Rev binding protein		201
combined receptor 1 (brain)	=	
ribosomal protein L14	•	
COMPANIES MACHOES DAMO 11454 (FEA=EST (AB_AREF=G11578817 /AB_AREF=G112A73x03.s1 /KLONE=IMAGE:S31268 /UG=Hs.258725 ESTS, Hoderstely similar to ATPO_HUMAN ATP ST AMOT 1454		1.07
produce the production of the		1.07
ATD KEN productuse 4, regulatory subunit 6 (636), defa isoform		1.07
reference (TMI) II (MA femoral A codemonial a 1 to Arbo		1.07
DAMICS prefair	KM_000938	1.07
IQA/02/6 protein	A8028990	1.07
	D87466	1.07

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Consensus includes gb./1867199 /FEA=EST /DB_JQEF=gi:S540214 //DB_JQREF=estwa01c11.st /CLONE=IMAGE:2296820 /V6=Hs.324787 solute carrier family \$ (inoxital transporter), me Alb67198	me A867198	1.07
CONSTRUCT TERRORY (1982) 11 (DE Eltomo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 708, 736E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 70E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 70E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEb=mBNA, 70E = d;10437841 / 10E = Homo saziens (DMV FUZ1690 fs., close (OL09538, FEB=mBNA, 70E = d;10437841 / 10E = d	d AK025343	6.1
DAZ associated protein 2	NM_014764	70.
hypothetical protein FU13798	NH_024773	.0
Persteldae lite 1	249258	1.07
hodocatocaylase synthetase (biodin-(propriomy-Coenzyme A-carbonylase (ATP-hydrobysing)) ligase)	NN_000411	.07
tumor necrosis factor receptor superfamily, member 10b	AF016256	1.07
wesicle-associated membrane protein 3 (celtubrovin)	80003570	6.5
hypothetical protein FU23209	NM_024895	1.07
endothelin receptor type A	581545	20.
RAMOA71 game product	86107203	6.0
Z.Sobigoadenytute synthetase 1 (40-46 tD)	NM_016816	1.07
small nucham RNA activating complex, polypeptide 3, 50kD	NM_003084	1.07
Dipartite motil -containing 15	AF220133	1.07
405 ribasamal protein 527 isotorm	NM_015920	1.07
Consensus includes gb/L137784 /DEF = Human DIAL sequence from clone RP1-19913 on chromosome 6 Contains ESTS, CSSs and Cp6 islands. Contains part of the gene for a novel pro AL137784	ro AL137784	1.07
serine (threatwise kinase 17a (except esis-inducting)	AW194730	1.07
mittoon-activated protein lanse (1	US3442	1.07
Propublish protein MC(10765	NM_024345	1.07
adenomical cohocas coli like	A.078616	1.07
maters [ 44 profession ]	224459	1.07
eddoin ( Jarma)	A763123	1.07
Pt donain certained 2 with 245 domain	A681013	1.07
destruction functional destruction Durberton and Rector from 1 includes DXS164 DXS266 DXS230 DXS239 DXS269 DXS269 DXS270 DXS272	NH 004010	1 07
phenohitic aid phonohitise hoe 2(	AF047760	1.07
sarrain demonate	AF047004	1.07
unerantino orday / (micropoda), proton caries	U94592	1.07
describes destruction on the first second of the second of	L13852	1.07
Section of the sectio	A735639	1.07
I many from the last of the la	NA 015936	1 07
Newton providence of the 20	KM 017913	1.07
PART & constitution (univ	AF112206	1.07
ctamicaling	A435828	1.07
A bisme (PLA) archer protein	U34074	1.07
handrove court bette theoretical is controlled	M60718	1.07
impurity of the property of th	NN 006903	1.07
of the foundation of the American Ameri	NH 007325	1.07
general respect to the control of th	A8032951	707
About and Carolina powers	NH OCEALS	107
The first family that	NN 02:065	6
A PARTIES AND	1963 FO MA	9 6
part 11 to 11 to 12 to 1	45070513	6
response response in the control of	X03348	1.07
monored to marrachine of films with the contraction of the contraction	NN 012329	1.07
IQA 168 protein	AX022610	1.07
Dirk Roger protein 117 (HPF9)	NM_024498	1.07
hypothetical protein FU10842	A278150	1.07
gD:N17561 (DEF=Numan HMC class il DQ-beta associated with DR-6, DQ-4) protein, complete cds. FEA=mRNA /GEN=HLA-0Q81 /D8_XREF=gi:188188 /FL=gb:H17565.1	M17565	1.07
innaktol 1,4,5-triphosphate neeptor, type 2	A963873	1.07
chloride intra-chlular channel 1	U85978	1.07
ABO blood group (transferase A. Apha 1-3-N-keny)galactosaminyltransferase; transferase B. Alpha 1-3-galactosytransferase)	761510	1.07
protein timase C. theta	L01087	1.07
papticlydycine alpha-amidating monoarygenase	A022882	6:
zint finger protein 197	166900 KN	.03
Las essectation (kaleDS/NF-6) domain tamty 2	NM_014/3/	6.6
uboquitin specifik processorie (Drosophila fai takeis related)	X4-00-6X	6.6
hypothetical protein HSC4707	KM_024113	6.5
mesodem geric trascriti hondog future:	MA_002402	6.6
DOWN TO THE ENDER DEPOSIT OF THE PARTS CONTROL OF THE CONTROL OF THE CONTROL OF THE PARTS OF THE	41915000	9 6
rigionacia promi n. 10 10/1/12 microbala modela de marcina de marc	AW242297	6
instructions—associated protein (	NH 020322	201

The factor ones	OCODO NIA	3
All the principles of the contract of the cont	NM 016311	9 6
vesigle executable emittees (cellularing)	Brinsa41	701
DQTP-4/12110 protein	NM 014034	10,1
insulin unstrum betar i	NA DITTI	201
abbest Afficient And Antonopada Chinese Ivas	178577	5
(Matterstring and East )	NA OUTBE	2 2
activity of the summer was	ME939675	6
rait-raited transcripton factor 3	AA541630	101
Pypothatical protain LOC35565	AF070568	1.07
chromosome 11 open reading frame 5	KM_014205	1.07
polymense (DMI divected), theta		1.07
Conserve includes go:AA927664 /FBA=EST //DB_XREF = gi:3076484 //DB_XREF = est:om71h10.s1 //CLONE=INMAE:152675 //UG=Hs,171626 transcription elongation factor B (SIIII), polypep	pep AMS27664	1.07
Neterogeneous nuclear ribonuciacymatein At	A1144007	1.07
Psychotical protein FU20136	NN_017684	1.07
bane earphogenetic protein 8 (oxteogenic protein 2)	NM_001720	1.07
prefetén I	NM_002622	1.07
hypothetical protein RU10956	NM_018283	1.07
stande-bapte-motatione, aptra polypeptide 1 (3-ozo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	AF113128	1.07
Cysteme-fich argogenic inchese, 61	AF003114	1.07
but those protein 220	NH_006766	1.07
IAN -essociated protein 3	NM_003933	1.07
of subsections to control in the con	A010395	6.
functional process for the control of the control o	099/10 <sup>-</sup> NA	6.5
ANTICLE STATE OF STAT	769600 PM	6.0
describes account of the following squeez core, for the country of	, CI ANUCOOUS	9.5
Innotherical protein E170359	RC000078	9 6
He production is the control of the	M38083	6.
cob() jackon orden vytodanic 3	NK 030979	201
CP Agents present stopped and the company of the co	NW DISCSE	6.
thects (Threat necess)	722551	107
067243.441750 protein	NN 015527	6
RAD9 homotog (5, pombe)	NW_004584	1.07
nitris caide synthase 24 (inducible, hepaticytes)	124553	1.07
solute carrier tarrity 25 (caractine/acyteamitine translocase), member 20	BC001689	1.07
hypothetical protein FU11336	KM_018393	1.07
protein imhibitor of activated STAT3	660900 NN	1.07
protein tyrocapatics, non-experiently autotrale	086043	1.07
Trape A merital relationship homotog 1	86025078	
Det. Triple M. O. Branch J. Patternin. S. A. Branch J. A. Branch M. Branch J. A. Branch S. Branch S. A. Branch S. Branch S. A. Branch S. Branch S. A. Branch S. A. Branch S. A. Branch S. Branch S. A. Branch S. A. Branch S. A. Branch S. Branch S. Branch S. Branch S.	A459274	6 5
Productive pretain [120005]	NW 017617	9 5
globlations amplified sequence	NM 001483	201
Aport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene i	AX023637	1.07
solute carrier tamity 25 (mitochondrial carrier, Analar), member 12	NM_003705	1.07
(OQ7 coenzyme Q, 7 homolog ubiquinone (yesst)	AF032900	90.1
nuclear receptor substantly 4, group A, member 1	D49728	99.
potassum voltago-gated Charmel, Shaw-maited sublimity, member 3	KN_004977	8 :
A STATE THE PROPERTY OF THE PR	NA_00155	8 8
during nucleated by the control of process of the control of the c	RE412795	8 2
(CANOS) protein	AI656706	3 2
sin3-associated polyperpide, 30t0	AF055993	8.
spandybapjahiysad dystkaia, lata, pseudogene	AF291676	9.1
transfocuse of outer mitochondrial membrane 10 homolog A (yeast)	8003633	90'1
myo-inosital 1-phosphate synthese A1	AL137749	90.1
glucoramine (N-acetyl)-6-authalase (Sanfilippo disease IIID)	NM_002076	90.
ubspatin perint protects 4 (proto-oncogens)	AF017306	8.
broad mineral	AN304674	8 3
Internation 1 of Necytor, april 1 international and a second seco	500 MM	<u> </u>
Impounds prouni Impounds prouni ELI/722	MM 024970	<u> </u>
Table 1 months and annually	017L30.EN	3.

TAI cytotoxic grande-associated RNA binding protein	H96549	3
hypothetical protein FU13593	NM_024780	8
endothelial cell growth factor 1 (platelet-derived)	NH_001953	1.06
arachidonate 12-lipoxygenase pseudogene 2	AF020774	9.
RABIIA, member RAS corcogene family	NH_004663	- 8
small inducible cytokine subtamily 8 (Cys-X-Cys), member 11	AF030514	8
Genetrylarginine dinathylaminohydrolase 2	AX026191	8.
Commensus includes de AUT 146809 FEA=EST (OB. XREF=q:11008330 (OB. XREF=q:140146809 KLONE=HEMB11001564 (VG=H5.287476 Homo supens oDVA FU12004 fs. clone HEMB8 AUT 146809	FU12004 fis, clone HEMBB AU146809	9.
CA2+-dependent activator protein for secretion	NH_003716	- 8
coffeein 13. H-coffeein (Near)	NH_001257	1.06
bipartite motif-containing 3	A119307	9.
aspartoscytase (antinoacytase 2, Caravin disease)	6+0000_HN	1.06
translocation chain-esociation membrane protein	8000687	9.
sorbig neah 10	NM_013322	9.1
rfrag finger protein 1	NM_002931	9.1
hypothetical protein FU23119	NH_024652	1.06
gamma-aninobutyric acid (GABA) A receptor, gamma 3	892208	9.1
enembrane-bound transcription factor protease, site 2	NH_015884	9.7
stornatin (\$BP72)-tite 1	NM_004809	9.1
novel protein	NM_017515	90'-
anned NJ	NM_004034	8.
hypothetical protein FIL23445	NM_025075	90.1
8-call CLAyrephoma 11A (zinc finger protein)	AF080216	8.
dynain, azonemal, heavy podypopicide 9	AF257737	8.
period homolog 1 (Drosophita)	AF022991	9.1
chromosome 18 open reading frame 1	AW008505	90.
hypothetical protein similar to preferentially expressed antigen of melanoma	NM_023013	1.06
polycystic lidney disease 2-like 1	NM_016112	90.1
maternally expressed 3	AF090934	8.
hypothetical protein DK72p5661133	NM_030938	8.
TQAOBO2 protein	AB018345	9.1
mannan-binding lactio serine protease ! (C4/C2 activating component of Ra-reactive factor)	017525	8.
phorbolin-Eille protein MDS019	8F508948	90.1
low density igoprotein receptor (familial hypercholesterolemia)	570123	8.
myosin, light polypapóde 4, altali; atrial, embryonic	A/133353	1.06
hypothetical protein FU20116	NM_017671	8.
popeye protein 3		8.
Cansansus includes gb.N.138761 (DEF = Human DNA sequence from clone RP 11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for		8
machen resident conclusion:	A040324	8 3
Brownsporter in depreciarative featement wins oncopene ligand, megakaryocyte growth and development factor)	059495	8 3
RECEIVE PROCESS AND SECURITY OF THE PROCESS AND SECURITY O	10 NA 01845	8 3
coactivator-essociated erginine methyltransferase-	MSS1784	8.
myeloid/hymphoid or musel-timeage testerms (hithoras homolog, Drosophila); translocated to, 2	0.727.79	8.
THE NEXT, CHARLES FOR ALL 10	200570	<u> </u>
erre (unadopk) sessenius (Andobode)	NH_01433/	8
CONTROLLES DANS SENT FOR THE TOTAL STATES OF T	6 8AC clone (1) 98/3K-A-6 A095896	8 8
NOVEL 1 AND THE STATE OF THE ST	579100V	<u> </u>
A series with process notice, encountry of the	909060 TV	8 8
the year protein	ACSA1118	8 8
Proposition of the proposition o	A541534	3 2
I province to the control of the con	UN 014163	8 8
inactors (malfrids)	44196245	3 5
characteristic containing (D), subunit § (equilon)	8575748	90
physic A4	NM_005227	96.1
splicing factor profine/ghutanine rich (polypyrimidine tract binding protein associated)	AV705803	8.
servick-Epotuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	196810_MN	90:1
nomeo box 11-tike 2	KM_021025	9.1
protain binase, cAMP-dependent, regulatory, type II, alpha	NM_004157	8.
1953 Larget gene 1	A8007457	90.
werein)	NN 004796	8
UM binding protein 17	NM 022897	9.1

nuclear resolor subtanily 0, oroup 8, member 1	***************************************	į
(DA)115 protein	M-0004/5	8 3
larin 8 receptor	NM 00330C	8 8
ATPase, H+ transporting hysosomal (vacuolar proton pump), member H	46077614	3 2
appritylylucosaminidase	MEANT	3 2
heat shock 70t0 protein 4	******	8 8
Nich-chucos-roadsted protein &	2000	3 :
mitochondul intermediate pessiciase	MM_016238	3
<b>CARACTER CONTRACTERS</b> colonomics I catalogic colonomic	050034	8:
Consequent includes adviced to the Consequence of t	NN_003859	8
Conservation of ALASTOS ASSAURT TO 100 (100 ALASTOS ASSAURT) 11 (ALASTOS ASSAURT) 100 ALASTOS ASSAURT TO 100 ALAST	12152738	9.
Address of the property of the	A343027	8
fractionary 2 formulae training	AX023924	8.
Informacia protein Held 179	KM_024340	96.
webprodistriano encretaria	NH 002514	96
Veside-essocialed membrane protein 1 (synaptobrenin 1)	AU150319	8
carbotypepticles 0	000000	
f-box and WD-40 domain protein 18	00000	3 3
dual specificity phosphatas (1 (RNA/RN) complex Linteraction	C+769C30	8 3
DK72 5446052 cretain	MM_003564	8.
solute carrier tarrity 16 (monocarbonylic acid transcentes) member 6	AC049943	8 :
Consequent includes the REGISTOR RELIEF OF THE CONTRACT OF THE	NM_004695	8
Ethinocompanies of the state of	743 8E549732	9.
and the second of the second party and the second of the s	AI872408	9.
and the second s	NM_006359	90.
Constitution of the state of th	NM_005597	1.06
H septimental management		8.
CONSORRES SOLIE FALS 11 FEAREST / DB_XREF =9:11513897 / DB_XREF = extrad18.403.11 / CLONE =IMAGE.3365668 / NG=Hs. 152939 Homo sapiens done 24630 mRNA sequence	ice BF448315	8
KLZ/admontas E18 19kD interacting protein 1	NN 013979	90
transforming growth factor, beta 1		8
Consensus includes gb.184340,1 / OEF = M. sepiens mRNA for lg light chain, variable region (ID.CLL001VL). /FEA=mRNA /GEN=lg VI, gene /PROD=inmunoclobulin light chain, variable region		5
antytosis, progressive homolog (mouse)		2
bridging integrator 1	45001383	3 8
Conservation of the contract o	WW1383	8 3
Chromopolish (myeloproliferative leukamia vins oncored lisand, messkanowa news) and described the control of th	Pa AU/3363	<u> </u>
protein tyrosine phosphetase, non-receptor type 2	/40760	8 9
provate dehydropenase klnase, isoenzyme i	DICE OF MIL	3 3
mannosidase, alpha, class 1A, member 2	מומסת"שוני	<u> </u>
emezin k2	00343064	<u> </u>
candidate tumor suppressor p33 IN6 1 homolog	44487062	9 8
LMP (Neucine-rich repeats and PO2) and no PO2 protein	NA OTRICE	3 3
decayribonuclease I-like 2	* 12010 MA	8 8
similar to hypothetical protein HNDs-2386	1/21207En	8 8
60M family receptor alpha 2	96530730	8 3
Commensus includes ch.AW 166925 FEA.EFT OR 18FF	C\$1/60	8
Candidate Lumar successor p3 11/61 horners of 23 11/61 horners of		8
Res essectation (Palificial Armin Tarmin)	KM_016162	8
HOLT Indian methyttamsterace like 1 S. converse	MM_00/182	8
cholimencie receptor, nicotivis, beta polymencide   (marcie)	KM_001535	8
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Consensus includes gb.AW274147 FEb=E57 DB_AREF=@i56661777 DB_AREF==strn34c08.a1 ATONE=INACE2695622 AG=Hs.270527 Homo sapient mBWK_CDM, DBF2b49460327 (HWZ9491)	0/700/ WA 4// (5/07/5/2	3 3
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hypothetical protein FU131S4	865720 KN	5 2
vesicle-associated membrane protein 5 (myobrevin)	NH DOCK34	2
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eularyotic translation initiation factor 2-alpha kinase 3	NM 004836	2
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Programmer Co-Cuntae/mucros-C, b-tophosphalase 2	KM_006212	3.
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hypodhetical protein MGC9084	AI 035369	5 2
hypothetical protein FU20039	NM 017635	2
caktum/calmodulin-dependent protein kinase (caM kanase) II beta	AF112472	3
hypothetical protein FU 10213	KM 015029	2
and these protein 75 (08/6)	96208M	3
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borness based as a fine of the first	PLACE 1011 AUI 57915	2.
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hypothetical protein FLI10815	W535244	<u>z</u>
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hypothetical protein FU12581	MM_024865
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## FIGURE 4D.

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nbooms protein L38	8(000603	4.47
killer eed immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	X93596	4.39
PTPRF interacting protein, binding protein 1 (lipnin beta 1)	N35896	
hypotherical protein FU12619	CEU25733	7
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cofactor required for 5p1 transcriptional activation, subunit 2 (150kD)	AK023368
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langai 1 (suppression of tumorigenicity 6, prostate; (OB2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody (A4))	NM_002231
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Terris protein	NN_022487
inhibin, beta (	NM_005538
reversion-inducing cysteine-rich protein with kazal motifs	AK022897
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growth factor receptor (TMR superfamily, member 16)	NM_002507
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hypoth	hypothetical protein FLI23548	NM_024590	2.41
flood.	hypothetical protein FU225S8	NH_022747	2.41
notes	nuclear factor UB	U70862	2.40
godili .	hypothetical protein My014	NM_030918	2.40
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anc fin	bit Anger protein 42 (meloid-specific retinois acid-responsive)	A1733248	238
chech	thectpoint suppressor 1	AA860806	2.37
protess	protease, serine, 21 (testisin)	NN 006799	2.37
fonded	popology arginine deiminate, type V	AF229067	2.37
calpain	calpain 9 (n(L-4)	A8038463	2.37
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Ephb3		X75208	2.37
craniof	cravidacial development protein 1	D85939	2.36
dopie	sidophorin (gpL115, leukosialin, (D43)	X60502	2.36
Consen	Consensus includes 90:K00627.1 /DEF=human kpni repeat mma (cdna clone pcd-kpni-8), 3 end. /FEA=mRNA /DB_XREF=gi:337653 /UG=Hs.203776 Human kpni repeat mma (cdna clone y K00627 Consensus includes go K00627 (Consensus	I K00627	2.36
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CGI-58 protein	votein	NM 016006	2,34
hypothe	hypothetical protein FU10254	NM_018041	2.34
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hypothe	brotheria profess [1143] 0	NM_004982	5 5
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calmodu	calmoduin 1 (phosphorylase kinase, detta)	H27319	232
leukocyt	eubocyte immunoglobulin-like receptor, subtamily 8 (with TM and ITIM domains), member 3	AF009643	2:32
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requent motion galded 24 (Figure 17) Mg Till Emerky 73405 s. (ALONE THAKE 27) 177 MG Till 25525 Norm speins milw. COM DOT 24344.19 (free of H4852 AND CONTROLL OF TILL STREET AND CONTROLL OF TILL STREET AND	DNA fragmentation factor, 45 kD, alpha pohypeptide	NM_004401	2.20
Autorization of protects, the test of the control o	receptor bytoshe lande-sits orbital receptor 1		5.19
10,002.00   Commonwed   10,000.00   Commonwed   10,0	CABA American Schools of Garles St. (FEETS) 1/06_ARTF=613Y 1/06_ARTF=613Y 1/06_31 (ALWE=1MARE;Z/917) /U6=14: Z8562 Homo supers miRNX CDNA DR Z9434A119 (Tron CABA American Camada)		5.5
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He demonsion requirements of the control of the con	hypothetical protain PR02900	NH_018635	2.19
Action of the contraction of the	dromosome 21 open nueding frame 62	965610 NN	5.19
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y destine processes 2 (gestrointerina)  Will 20233  Will 20235  Wi	Found cell achterion molecule 2	NW 004540	2 18
ALMOSTO protein introduction protein market of the control of the	glutathione perunidase 2 (gastrointestinal)	NM_002083	2.18
matria matrial matrial protection and the control of the control o	KUMG170 protein	A808958	2.18
brighting interface to (1900-85) and obtained a control of control	introdulular by duronan-binding protein	AF241831	2.18
Antities of section contropic, labrate 4  antities of section control and section and RN (COLV D072-0667HO46). FELamRNA / EEH=D072-0667HO46 (PROD=hypothetical protein / DB_A 14.513703)  M11167 Name 255 ANA sequence, langth 5025 bases, 3 prime larget bases 3311-4995  antities of the control of the contr	Martin metabological and (stromelysin 2)	NM_002425	2.18
inscription by monocloud antibody NRC 02.2  Consensus induces guild S10.2011. (NEE Homo superiors mRLV, CDN UNIZEGENHOLE), FEAL mRNA /GEN=DIGID-657HOLE /PROD=hypothetical protein /DB J. ALS1203  AN 11167 Name 255 ANA sequence, length 50.203 bases, 3 prine layed bases 3331-4995  soldes carrier family 14 (and broughouts). (Mod blood group)  AN 11167 Name 255 ANA sequence, length 50.203 bases, 3 prine layed bases 3331-4995  soldes carrier family 14 (and broughouts). (Mod blood group)  Consensus includes go. ALS0 1.005 Februar ageins OUN. FIL21419 fst, clone (OLO0303, REA=mRNA /DB_JREF=gi:0437312 /UG=Hs, 306799 Homo supiens OUN. FIL21419 fst, clone (OLO0304, FEA-mRNA /DB_JREF=gi:022201 /UG=Hs, 140402 Homo supiens OUN. FIL21419 fst, clone (OLO0304, FEA-mRNA /DB_JREF=gi:022201 /UG=Hs, 140402 Homo supiens OUN. FIL21419 fst, clone of COLO0434, FEA-mRNA /DB_JREF=gi:022201 /UG=Hs, 140402 Homo supiens OUN. FIL21419 fst, clone of COLO0434, FEA-mRNA /DB_JREF=gi:022201 /UG=Hs, 140402 Homo supiens OUN. FIL21419 fst, clone of COLO0434, FEA-mRNA /DB_JREF=gi:0022701 /UG=Hs, 140402 Homo supiens OUN. FIL21419 fst, clone of COLO0434, ARN /DB_JREF=gi:0043749, ARN /DB_JREF=gi	orderants recently inchronic laints of	MM_016293	2 .
Consensus includes gb.MS.1200.1. //OFE inhome supriors supriors mRNA. Gall Month (Fig. Months gb.MS.1200.1.) //OFE inhome supriors supriors mRNA. Gall Months gb.MS.25 bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument, langth SS.25 bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument, langth SS.25 bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument, langth SS.25 bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument, langth SS.25 bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument, langth SS.25 bases, 3 prime trapel bases, 3 prime trapel bases 3.311-4395  ANTITES NAME accument includes gb.MSG.14.2. //OFE inform suprime cloud. FLIZ149 fit, chem (COLOGAS, FELE-mRNA FELE-ELIZOGAS) ANTITES NAME ANTITES NAME ANTITES NAME accument includes gb.MSG.14.2. //OFE inform suprime trapel protein for the supriment of the suprimen	arigan identified by monocloud articles (N. C.).	H23979	2 2
H 1167 Houng 125 MM sequence, lamph 2025 bases, 3 prime larget bases 3331-4995  NH 1167 Houng 125 MM sequence, lamph 2025 bases, 3 prime larget bases 3331-4995  Souther carrier brailty 14 (rear brange) 414 (rear brange) 400 decorption)  Consensus includes gb-M2025072, 10FE shown supiens CDNk FLI21419 fb, chone COLO4084, /FEA=mRNA //BL-M2FE=gi:10437512 //LC=Hs. 306759 Homo supiens CDNk FLI21419 fb, chone COLO4084, /FEA=mRNA //BL-M2FE=gi:10437512 //LC=Hs. 306759 Homo supiens CDNk FLI21419 fb, chone COLO4084, /FEA=mRNA //BL-M2FE=gi:10437512 //LC=Hs. 306759 Homo supiens CDNk FLI21419 fb, chone COLO4084, /FEA=mRNA //REH=LI20663 //RC=Hs. 306759 Homo supiens CDNk FLI21419 fb, chone MANHALO20931, mRNA //REH=mRNA /	Consensus includes gb:ALS12703.1 DEF selfons supiers mANA. cDNA DK725657H046 (from clone DK725667H046). FEA=mRNA /GEN=DK72667H046 /PR0D=hypothetical protein /DB.	X ALS12703	2.18
NH, DISSES Consensus includes gb-MX001447. (DEF Ellown supiens OUN; ELIZ1419 ft, chone COLO4034, FEB-mRNA NB, MEF=g; 10437517 ALC=Hs, 306759 have supiens OUN; ELIZ1419 ft, chone OLO4034, FEB-mRNA NB, MEF=g; 10437517 ALC=Hs, 306759 have supiens OUN; ELIZ1419 ft, chone OLO4034, FEB-mRNA NB, MEF=g; 1022701 ALC=Hs, 306759 have supiens ONN; FLI010580 ft, chone NLT10580 ft, cho	H11167 Human 225 ANA sequence, length 5025 bases, 3 prime larget bases 3331-4995	M11167	2.18
Consenses anches governot (LOCE Incidented and Paris) of the Consenses anches governot (LOCE)	souths carrier thanky I (was harsporter), member 1 (fold blood group) formatted a hardporter) in special control of the contro	KM_015865	2.17
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solver carrier tanky 9 (bodium/progen archange); indram 2  solver carrier tanky 9 (bodium/progen archange); indram 2  solver carrier tanky 1 (bodium/progen archange); indram 2  solver carrier tanky 1 (bodium 2  solver carrier tanky 2  solver carrier tanky 1 (bodium 2  solver carrier tanky 3  solver carrier tanky 4  solver carrier tanky 6  sol	GA0341 protein	AW139448	71.7
ga/MG_1744.1 Off Enhann sapient inpodencial protein EU2005.3 (FLICOOS.3) mRVA, fight=FLIZOOS.5 PROD=hypothetical protein FLIZOOS.5 (FLIZOOS.3) mRVA, fight=RLIZOOS.5 PROD=hypothetical protein FLIZOOS.5 (FLIZOOS.3) mRVA, fight=RLIZOOS.5 prod=hypothetical protein FLIZOOS.5 (FLIZOOS.5) mRVA, fight=RLIZOOS.5 prod=hypothetical protein Frainch Profes. Lil. 35105 gaig prosphoprotein 4  RVA (1212) Fin. clone RP-45(713) on chromosome 1442.2-43. Contains an enclase 1. (alpha) (EMO) praudogene, the gene for Poofs. LLI 35105 gaig prosphoprotein 4  RVA (1212) Fin. clone RVA (1112) Fin. clone RVAMAINOODOS, fFEL=mRVA, fOB_XREF=gi:10437519 (MC=Hx, 38812 Home supiens cDNA FLIZIST) Fin. clone RVAHAINOODOS, fFEL=mRVA, fOB_XREF=gi:10437519 (MC=Hx, 38812 Home supiens cDNA FLIZIST) Fin. clone (2014) Fig. Clone RVA (1112) Fin. clone (2014) Fig. Clone RVA (1112) Fin. clone RVA (1112) Fin. clone (2014) Fin. clone RVA (1112) Fin. clone (2014) Fin. clone RVA (1112) Fin. clone RVA (1112) Fin. clone RVA (1112) Fin. clone RVA (1112) Fin. clone (2014) Fin. clone RVA (1112) Fin. clone (2014) Fin. clone RVA (1112) Fin. clone RVA (1112) Fin. clone (2014) Fin. clone RVA (1112) Fin. c	solute carrier family 9 (sodiun/hydrogen exchanger), isotom 2	AF073299	2.17
gar95421 (DE Eleman superary   Lappa Egit chain variable region 708, XEE = 108291  gar95421 (DE Eleman superary   Lappa Egit chain variable region 708, XEE = 108291  gar9 phosphoprotein 4  Canasara inchdes ga.X.(136105 OEE=Human DN sequence from chone RF-L6706 13 on chromosome 1q4.2.4-3. (contains an enclass 1. (alpha) (ENO)) passedgene, the gene for Pode 1. (136105 gar9 phosphoprotein 4  Canasara inchdes ga.X.(22219 1.0EE=Human DN sequence from chone RF-L6706 13 on chromosome 1q4.2.4-3. (contains an enclass 9. (alpha) (ENO) passedgene, the gene for Pode 1. (136105 MR) of 18. (2012 13105 MR	GONN 10164 NOT September Supriment Mypotherizal protein FU20063 (FU20063), mRNA. FEA=MRNA FEN=FU20063 /PROD=hypotherizal protein FU20063 //DB_XREF=g1:8923068 //UN	: NM_017648	2.17
gody prostriction of your content of the content of	COURSE 11 (VEX.E. From supering that the wanthe region (VILX) milk), complete cas, IFELMRIA (EKE-VIII.X2) FR00=1g Lape light chain variable region (VI). REF.	. 096291	2.17
Compensa includes go.X0022219.1 DEE=Homo supiers CDNA FUL2157 fs., clone HAMMA1000500, FEB=mRNA, 708_XREF=gi:10433569 7/0c=Ht, 38812 Homo supiers CDNA FUL2157 fs. MX022219 interfacing in Local Compensation in Local Compe	comments in the mount of the control	. AL136105	9 7
interlucion 1, beta Consensus includes gas/MO25077.1 /DEF = Homo supiens CDIV. FUZ1424 fb., clone COLOMIS7. /FEA=mRM, /DB_JXEF=gi:1047749 /UC=Hi, 280F622 homo supiens CDIV. FUZ1325 fb., chone COLOMIS7. /FEA=mRM, /DB_JXEF=gi:10477474 /UC=Hi, 280F502 homo supiens CDIV. FUZ1325 fb., chone COLOMIS56. /FEA=mRM, /DB_JXEF=gi:10477474 /UC=Hi, 280F502 homo supiens CDIV. FUZ1325 fb., chone COLOMIS56. /FEA=mRM, /DB_JXEF=gi:10477474 /UC=Hi, 280F502 homo supiens CDIV. FUZ1325 fb., chone consensus includes gas/FES3251 fb., chone consensus con	Consense includes go-XW22219.1 (DEF = Home supers CDNA FUL15157 fs, clone MAHAN 1000500, FEA=mRNA /0B XREF=cs;1043359 /06=15, 98812 Home susiens cDNA FUL15157 Consense includes go-XW22219.1 (DEF = Home susiens cDNA FUL12157	KM_U14498	2.16 2.16
Consense includes gp.MO25077.1 DRE Home supries DNV. FUZ1824 fs., clone COLO4157. FEB=mRN. DB_XRE=gi:10477519 /UG=Hs.287662 Home supries CONK. FUZ1828 fs., chore COLO4157. FEB=mRN. DB_XRE=gi:10477519 /UG=Hs.287650 Home supriess CONK. FUZ1835 fs., chore COLO4157. FEB=mRN. DB_XRE=gi:1047747 /UG=Hs.306720 Home supriess CONK. FUZ1835 fs., chore COLO4157. FEB=mRN. DB_XRE=gi:1047747 /UG=Hs.306720 Home supriess CONK. FUZ1835 fs., chore COLO4157. FEB=mRN. DB_XRE=gi:1047747 /UG=Hs.306720 Hr.206720 HR.206771 HR.206720 HR.206720 HR.206720 HR.206720 HR.206771 HR.206720 HR.206720 HR.206720 HR.206720 HR.206720 HR.206771 HR.206720 HR.206720 HR.206720 HR.206720 HR.206720 HR.206720 HR.206720 HR.206771 HR.206720 HR.206771 HR.206720 HR.206771 HR.206720 HR	interholdin I, beta	M15330	2.16
Commence includes gip. MOSSOS I. (DEF Home supers 10NY: FUZ1385 fs., close (010335s., FEB-miNN, AD JREF-agi:10437474 AlG=Hs.306750 Home supers 10NY: FUZ1385 fs., ch. AU025038 mingram-activated protein bissus a linearching protein 2.  NEX. Section 1. (Section 1. Section 1. Se	Consumus includes gb.W025077.1 /DEF = Homo supiens cDNX: FU21424 fis, clone CO104157. /FEA=mRNA /DB.XREF=qi:10437519 /UC=Hs, 287662 Homo supiens cDNX: FU21424 fis,	. AK025077	2.16
INFORMATION OF THE STATE OF THE	Conservation behavior spAVQ2503.1 (DEF whom septions cDNV: FUZ1355 fs., chose CQL03356. FEA=mRNA /DB_AREF =gi:1043747 /UG=Hs. 306750 Homs septions cDNV: FUZ1355 fs.,	. AK025038	2.15
conseque monotor parts 700_ANE set 179323 00_ANE set 1659321 ACONE INAME 44691 / Vice 151 180513 AIP-binding cassette, sub-lamity A (ABC), 1659321 AND binding cassette, sub-lamity A (ABC), 1659321 AND binding binding by the set 1730 AND binding by the se	Antigen-activated process lanses & interacting protess &	NM_016431	2.15
National Parties acting protein National Authority of Market and Authority of Market Section 1970 of Market Sectio	MOTERATE MATERIAL INVESTIGATION IN THE CONTRACT AND THE CONTRACTORS AND THE CONTRACT AND TH	BF693921	2.15
Potassium inversity-rectlying channel, subtanity I, member 5 solute carrier tamity I (gital high affinity glutamate transporter), member 2 HH_004171	herestopoietic Platestration protein	Allakses	
soldite carrier family   (gial high affinity glutanate transporter), member 2	potassium inwardy-rectifying channel, subfamily I, member 5	NM 000890	212
L71		NM_004171	2.15
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	series Physiciae linus 6	NM D03158	2.15
	veril - I marine leuternia viral concorner hornologi	A/088622	2.15
	UDP-4-alberackNx beta 1,3-quartron/transferaxe, pohjpeptide 3	AB050855	2.15
	Consumsus includes gb.XIV756729 /FEJA=EST /OB XREF=gi:10914577 /OB XREF=est:AV756729 /CLONE=BMCACB11 /UG=Hs.317661 ESTs	AV756729	2.15
	SHB adaptor protein (a Sor homology 2 protein)	KM_003028	2.14
	pleiomorphic adenone gene 1	NM_002655	<b>7.</b> 14
		A760053	7.7
	PD2 domain containing guanine nucleotide exchange factor (GEF) 1	AL117397	7.7
	Consensus includes gb.1MP371254 F.EL=EST (AB_LXREF=gi:8161099 //AB_LXREF=est:EST383343 //VG=Hs.178433 ESTs	AW971254	<b>5</b> .14
	omo sapens mKNA: CDNA DNF CDSABLO120 (from clone DNF CDSABLO120). /FEA=mRNA /DB_XNEF=9:+8884366 /UL=H3:98314 Homo sapiens m		71.7
		NM_000439	7.14
	as and steroid delta-isomerase 2	KM_000198	71.7
	gense 3 lanty, member 8 l	80002553	<del>-</del>
	Xen	AX026120	7.7
		000589	¥ ;
		KM_005388	<u>.</u>
	wator, undanase	NM_002658	7
		NM_001638	7 :
	general ansartorior, tayon/populoe 3 (340) subunit	A369458	3 :
		NM_013984	3 :
	om syde progresson og protein. Sem syde progresson og protein.	NM_004/45	3 5
	14717	AK073017	3 5
	RJAW996 protein	AA909765	2.13
	hypotherical protein FU11155	NM_018342	5.13
		NM_024823	2.13
	zinc Knyaw protein 236	AK000847	2.13
	(crounisms includes gb.XU1 46646 /FEAT 70B_XREF = gi.1 1008167 /DB_XREF = ssi.XU1 46646 /KLONE=HEMBB 1001096 /VIG=H: 179752 Home supiens cDNA FU10270 fs. clone HEMBB AU146646	AU146646	2.13
		NM_006548	2.13
	ine kinase, receptor, type 3	NM_002530	2.13
		AK002207	2.13
	d buxen)	NM_017569	2.13
	1, anistrock	NM_001399	7 :
	Approximate to the state of the	MM_002643	7 .
	A copting demonstrate the Authority	MM 000726	
		181001	2 2
	member 2	A1189305	212
		NH_017736	21.2
	bas pohjpeptide 34	NH_014681	2.11
	member 16	NM_016945	11.7
		NH_013361	<b></b>
	especific anyogeness inhibitor 3	18011122	- 7
	COMPARAD STANCK-COSU (FEXTEZ) FUB_MIEF = G1:2681224 FUB_MIEF = G1:2681234 FUB_MIEF = G1:26828 FUGEE	AUG42030	17
	m chromosome resion 23	NA 025042	= =
	apiens cDNV. FU21442 fis, clone COL04429. highly similar to HSA237839 Homo sapiens mRNA for hypothetical protein. FEA=mRNA (DB	W025095	-
	petched homolog (Drosophila)	AL044175	2.11
	K670547.1 / DEF=Hama sapiens dane 24820 mRNA sequence. /FEA=mRNA /DB_JSTEF=g;3387909 /UG=Hs.146312 Hama sapiens dane 24820 mRNA sequence	AF070547	11.2
		AF116674	<b>5.</b>
	ONE AS AS CONTROL OF A CONTROL	AL080170	= :
		047710	Ę:
	/DB_XREF=qi:3841728 /OB_XREF=est:qu3910.x1 /CLONE=IMAGE:1967179 /UG=Hs.248999 ESTs	W246331	7.17
		NM_002898	7.1
	135	NM_030936	2.11
		NM_021638	2.11
	N 2 STEPHING STORY OF THE PROPERTY OF THE PROP	KM_025235	5.10
		NM_018629 RG434168	0 5 5
	(mencarbarylic acid transporters), member i	85511091	2 2
	protein ligase, clone MCC:2079, mRNA, complete cds. FEA=mRNA /PRO0=Similar to Nedd-4-like ubiquitin-protein liga	(000108	2.10
L	pregiums specific beta-1-dyscopratein 3	132065	2.10
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proported proceed must 3) to NOV entering: DA binding enterin 2	701020	-
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Wire time !	C75564	7 .
CDC14 cell Géraion cycle 14 homolog (8 (S. cerevisiae)	RF792631	; ~
interleution 13 receptor, alpha 1	062858	2.5
homeo bos (S	KM_018953	7.1
dipoptiohypedictor IV (CD26, adenosine deaminase complexing protein 2)	M80536	7.1
basis helis dopphelia domain centaining, class B, 3	8E857425	2.1
Inacher Collins-Francescheffi syndrome I	AW167713	2.10
entrellements +	063412	₹ ;
proving and an artist and artist artist and artist artist and artist	MM_016171	5 2
hypothetical protein PRO1544	NM D18586	3 8
ATPase, H+ transporting, hysosomal (vacuolar proton pump) 940	A/25/2582	
Consensus includes gb.AV753204 /FEA=EST /08_XREF=gi:10911052 /08_XREF=est:AV753204 /CLONE=WP080808 /UG=Hs.170267 ESTs		2
Comments includes go XF052160.1 (DEF = Home sepiens done 24629 mBNA sequence, /FBA=mBNA /DB_XREF=gi-3360471 /UG=Hs. 142570 Home sepiens done 24629 mBNA sequence		2.0
depoleration ( )	W79394	20.0
ALA INSTINUTION AND INTERFERS A METALITY BULL AND ALL ALE FEED OUR BORDWITH AND ALL ALL ALE AND AND AND ALL AND AND AND AND ALL AND		20.
general place remains appears, come not 1970c, mana, compete cas. // CA=mana // ROU=unitroom (protein for Ruc: 1976.) // Ubs_ARCF =gr: 1509/626 // Ubs=Hs. 306969 Homo sapar		2.0
Frontier sections of styles	AWEASA92	2 6
fbroblast growth factor 17	NM 003867	20.
Corporates includes gb-XX022192.1 /DEF=Home supiens cDNA FU12130 fs, clone MAHMA1000251. FEA=mRNA /DB_XREF=gi:10433534 /UG=Hs. 319567 Home supiens cDNA FU12130 tNG022192	30 · AK022192	2
hypothetical protein FU22670	NM_025144	2.0
hypothetical protein LOCS/187	86403671	0.2
CONSTITUTE INCOMEND FOR THE POST OF THE STATE OF THE STAT	AA017093	20.
TOTAL TO THE STATE OF THE STATE	U80987	20.0
(QAO) 19 are product	M92334	3 6
sylabdinase (N. influenzue) homolog	AA777793	20.2
cultins	NM_003478	2.08
Compensus includes gb.AXC01065.1 (DEF =Homo supiens cDNA FU10203 fs, clone HEMBA1004930, moderately similar to 265 PROTEASONE SUBUNIT 558. FEA=mRNA /DB_XBEF=gi:7022 AXC001065	322 AK001065	2.08
VAN CONCOUNT ALL AND WATER AND	NM_003371	2.08
Sections of Section 2015 (Section 2015) (Section 20	AM AV684859	80.7
Commensate includes aboV025552.1 (DEF=Homo seniors cDAN: FLI21899 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21898 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21898 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21898 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21899 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21899 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21899 fis. close PFPD3467, AFA==#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21899 fis. close PFPD3467, AFA=#RM, DR XBFE=#:10478101 AHC=Hs 306815 Home seniors ADM: FLI21899 fis. close PFPD3467, AFA=#RM, DR XBFE=#INTOXECO.	A AKO25552	3 2
CONDENSIS INCOMES 40:86433489 FEAREST NO. XREF = \$\psi 1333995 NO. XREF = \$\psi 133395 NO.	66433489	2.07
COTHERNIA MACHORS 9D-JU 050204.1 / DEFEMENDO SEQUENT (DIVING TOWN DIVIZOSSEF 1223) (from clone DIVIZOSSEF 1223). IFEX=MRNA /DB. JREF = 91:488443 / DG=HS. 28540 Homo sepiens in ALOSO204	1 n AL050204	2.07
Oraclasherouse protein 8 (five membrane-spanning domains)	A636233	2.07
dual cristica i	A-113018	70.7
(6-14)	RC28C017	9 6
cavadin 2	AA150110	9 6
dopamine megator 02	\$62137	207
IAM 1644 protein	AL047020	2.07
commensus includes go-Mu22892.1 /DEF=Hormo staplens cDNA FU12830 fis, clone MT2RP2003073. /FEA=mANA /DB_XREF=gi:10434549 /UG=Hs. 123158 Homo staplens cDNA FU12830 fi AND22892	n f AK022892	2.07
bounded of mounts RBP, 3 industrials income	NH_006780	2.07
defined defined consistent of transfer and t	A8015331	2.07
Consensus includes do AF 1952; 1 (AFE = Homo sasiens RT-LI mRNA, complete secuence AFE = mRNA (PRO)=RT-LI (MR XRFF = mi-13101AA ME = 4.35775 Homos sasions RT-LI me NA		9 6
coredinding textor, next domain, alpha subunit 2; transforated to, 1; cyclin D-related	NM_004349	20.2
alpha-k-glycoprotein 1, sinc	090427	2.07
ubiquitin protein liguae E.M. (human papilloma wirus E6-associated protein. Angelman syndrome)	8F588511	2.06
The state of the s	NM_020359	% %
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Museus annows governors, 1, 100° renorms agents for Luth's Links L	gi AK022023	90.7 7.00
plectorial homology-flat domain, tarrity A member 1	NM_005920	8 8
cytochrome P450 palypapide 43	20000	3
	A-280113	200

tuffalia-interaction protein	NM_012143 2.06	v
(1928)  (Transit Batter menyllaterises-like 1) S. Serevisias)  (Transit Batter menyllaterises-like 1) S. Serevisias (1928)  (Transit Batter menyllaterises (1928)  (Transit Batter menyllaterises (1928)  (Transit Batter menyllaterises (1928)		φ.
Augments in the second of the control of the contro		٠,
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90-U79250.1 (OEF = Human syrand-3-phosphate dahydroganase mRNA, complete cds. /FEA=mRNA /PROD=gyrand-3-phosphate dahydroganase //J8_XREF=gs-1806627 /FL=qb-U79250.1 U79250		9
CONSTRUCTION INCLORES OF ALCOHOLDS AS I NOTE Horm septions milliN. CONA DOP'25-SC40193] (from done DOP'25-SC40193). FELA-milliN ADS, CREF-ag-1499993 /UG=Hs. 3020-48 Homes septions in ALOH925-2.		9
Acceptate forces gov. 1995 / 1912 = Human DNA sequence from clone 17015 on chromosome K/Q22.3-24. (cntains an HMCI (high-mobility group (nonhistone chromosoma) protein 1) ALG35667 intermediate shared modelly group (nonhistone chromosoma) protein 1) ALG35667	AL035067 2.05	ς.
K4 and SE 1 interaction contains	NA_030/86 2.05	Λ,
gycoprotein IX (platets)		
KDA1102 protein		
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hypotherical protein FU21290		· •
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CONSOURCE STANDERS OF AT EEE TO BE VIETE = 1:853409 / 108_XIREF = extryi8 lh 12.1 / CLONE = IMAGE: 145703 / UG=Hs. 287419 Home sapiens cONA FULL SOS As, clone HEMBA 1002 I R78299		
stable and bredeny by the lettin S	830	~
Activation (15 = X03453 /DET = Bacterophage P1 are recombinase protein corresponding to nucleotides 581-1001 of X03453 /LEN=1058 (-5 and -3 represent transcript regions 5 prinx X03453		<b>د</b>
Communication of the CAME AND	•	
007.1 (DEF = Home statione IMAGE 26186, mRIA sequence, FEA= mRIA COR IRFE = mi-13407345 AIG= Ht 13745 Home sequence on the Ell 1427 A.	KM_UIBI14 2.04	
addein 2 (Peta)	55	
enclase 1. (alpha)		
dhomosome I open reading frame 6	AK023354 2.04	_
interferon induced transmittence protein 1 (9-27)	AA749101 2.04	_
Consents includes you's 2/21 (Oth Ethoma speems mRNV, clone: RES4-16, /FEA=mRNV, /OB_XREF=gis464187 /UG=Hs.174225 Homa supiens mRNV, clone: RES4-16 home-many-many-many-many-many-many-many-many		_
Improved prior 1 (1973)	62	
Proodbefical protein Page 1, 1991 1991 1991 1991 1991 1991 1991		
Character sonatonamotopin harmone-like 1	NA_U18600 2.04	
l-box and leucine-rich repeal protein 11		
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hypothecia protein 1-12028-4	744	_
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hypothetical protein FU20034	•	
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syndhome b-245, but polypeptide (chronic granulomatous disease)		
CONTRACTOR DATE (ALC TO THE SET T		
Internativation of the control of th		
testis specific antyrin-Bas protein 1	NM_02505/ 2.03	
cyclic muchacida gated channel alpha 3	60	
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Commence includes the \$54,000 FELEFOL DAY 1955		
some domain, immunodobulin domain (Pc), short best domain. Secreted (semandonin) 15		
small inducible optables subfamily A (tys-(ry), member 16	KM 004590 2.03	
Impotantie nuclear factor 4, alpha		
Conservate includes go AL390026 / DEF = Human DNA sequence from clone RP3-336/20 on chromosome 6 Contains parts of 2 genes for novel proteins, ES1s, STSs and 655s / FEA=(DS / DB_	ور	
Incomparison of the second of		
National control (1825)	539	
myonin, heavy potypaption 13, startula muscle	047674 2.02	
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Establishment of H. Connection of the Connection		
QA1016 protein	W7_006258 2.02	

Consensus includes gb.AL390857 (DEF=Human DNA sequence from clone RP I   51H22 on chromosome 13 Contains ESTs, 5TSs and 6SSs. Contains an HHRPA1 (heterogeneous nuclear riso AL390857 midden 2	2.02
s includes th ALSSS 1. OFF prices with the CDM DKPAR 100-20 from close DKPAR 100-20 ACC FROM STATES AND TREE military.	202
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is brancher 4	20.
. I DEF ≡Homo saziena cDNA FLI208%4 fis chore ADKAD1341 / FFA=mRNA //R XRFE=ni-7021185 //IG=Hs 306412 Homo saziena cDNA FLI20854 fis cho	20.2
stante-alpha motif and lexiner bipper containing lainase AJK	2.01
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hypothetical protein	2.01
Comensus includes go AL09435.1 /DEF = Homo supiens mRNK c ONA OK72658680220 (from clone DK72658680220). FEL=mRNA /DB, XREF=qi-4500218 /UG=Hs.170056 Homo supiens AL049435	10.2
glutamate receptor, metabotropic 1	2.01
heparan sulfate (placesamine) 3-0-sulfotransferase 1 NN_005114	10.2
	10.2
	<b>5</b> .01
WY domain binding protein 4 (formin binding protein 21)	2.01
coucts gall35958.1 /DEF=Hama supiens miNN. CDNA DNE 20547N163 (from clone DNE 20547N163). /FEA=miNA /DB_XREF=gi:8655637 /UG=Hs.306511 Homo supiens mi	<b>5</b> .01
SP2910 KN	2.01
osome 6q25.1-25.3 Contains a pseudogene similar to HMG (high mobility group) protein, S	2.01
injunctation or management (unional normoleg, unotophila); transcented to 10 Vol. 10 V	5,5
-	2.5
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one seriens PROJOJB mRNA. complete cds. AFA= mRNA. ARON=PROJOJ3 MR. XBFE=mi-1710054. Ali:=Hs 30A573. Home seriens PROJOJ8 mRNA. complete cds. (	8.8
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heart of the state	8.7
denaments account grown 1962-91 (No_Anter Spi 100 / 1/23 / 100 - Anter Spi 100	8.8
ndoblelia maker 2 pracursor	8.5
DEF=Homo sapiens (DNX FU23194 fs. clone REC00490, /FEA=mRNA //DB XREF=m; 10439802 //JG=Hs. 3106887 Homo sapiens (DNX FIL23194 fs. cs.	3 8
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arre 5	8.2
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mont immersions 2.5 percovers like ( notes of	8 8
ee FAP protein mRNA, partial cds. /FEA=mRNA /PROD=FAP protein ////// XREF=pi:1890646 /JIG=Hs 166101 Human putative FAP prote	8 8
Consensus includes gb.A.M.01963 (FEB=EST 708 AVEF = 61:2055965 AVE	8 2
Conserved includes go.W.257099, NOFE-Home supriens profity masin alpha (PTMA) gene, complete ces /FEL=(DS /DB_XRFF=gi:2017944 /UG=Hs.283947 Home supriens profity mostin alpha AF257099	8.~
very loss destristy geoprotein receptor	1.99
ma, clone MGC:12257, mRNV, complete cds. FEA=mRNA /PROD=Unknown (protein for MGC:12257) /DB_XREF=gi:13528866 /UG=Hs.326711 Homo sapie:	1.99
	1.99
Workly recipion and promine (V08784)	<u>8</u> :
DONOCO 1941 (DEF EHORRO Septens CONN FUZIS41 hs, clone COLOGIGG. FEAE INRIA (AB JATEF egi: 10437657 (AGE Hs, 306784 Homo sapiens CONN-FUZIS41 fs), cf	1.99
( Annual List Annu	66.1
Comments recover (Tructs) (1967) Active (1967) Active (1967) (196	66.1
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ytic (Includes spherocytosis, clinical type I)	8

	NA 016948	
tryce functional domain (PTRE interacting)	AL161955	8.
Consensus motiodes go./NOZ69131 (DEF = Homo supiens CDNA: FUZ3260 fs., clone (OLO5804, highly similar to HSU90911 Human clone 23652 mRNA sequence. FEA=mRNA (DB_XREF=g AR026913	nRNA sequence. /FEA=mRNA /OB_XREF=g AK026913	1.98
**** Surroma (Schmidt-Ruppin A-2) wind oncogene homolog (anan)	NH_005417	1.98
potassium voltuge-galled channel, Shab-related subfamily, member 1	102840	1.98
FLOOR ENGINE (SECU.)	81×26N	1.98
Contains included go.AL031224 (DEF = Human DNA sequence from clone 336H9 on chromosome 6p12.1-21.1. Contains the alternatively spliced TFAP2B gene for transcription factor AP-21 AL031224	TFAP28 gene for transcription factor AP-2 I AL031224	1.98
t protein-cupied receptor 20	NM_005293	1.98
Sopoulou (second)	NM_016445	1.98
source Larrer Tarry 10 (socium/bite acid cotransporter (amity), member 1	NM_003049	1.98
usual 69/09-96/27 Avo	AA902326	1.98
CORRESTANCE SPACE OCCHECA 1 (DEF = Home supiens mRNA, eron 1, 2, 3, 4, clone: RES4-244, /FEA=mRNA /DB_XREF = gi: 1843395 /UG=Hs. 104258 Home supiens mRNA, eron 1, 2, 3, 4, clone: RES4-244, /FEA=mRNA /DB_XREF = gi: 1843395 /UG=Hs. 104258 Home supiens mRNA, eron 1, 2, 3, 4, doctored for the control of the c	04258 Homo sapiens mRNA, expn 1, 2, 3, 4 AB000464	1.98
CONSTITUTE INCLUDES BOUNDESCENT. I DEF EHOMO SEPRENT DIVE FULZ 3014 fis. clone LNG00806. IF EA = MRNA /DB_XREF = 0:10439568 /UG=Hs. 306862 Homo septens cDNA. FULZ3014 fis. clone LNG00806. IF EA = MRNA /DB_XREF = 0:10439568 /UG=Hs. 306862 Homo septens cDNA. FULZ3014 fis. clone LNG00806.	6862 Homo sapiens cDNA: FU23014 fs. cl AX026667	1.98
angiopoletin-like 2	80710 MN	86
rabaptin-5	NH 004703	86
transcription factor 7 (T-cell specific, HMG-box)	COCCOO MM	90
KDADG69 gene product	202500_AM	96.
periodyl-pravi isomerase ( (cyclophim ()	6//BIO_MN	S
enhance of assertion (Concordia)	AW340/88	86.
Consensus includes 00-XLS-54245 FEA-EST (INB. XRFF = wr.12844837 (INB. XRFF = wr.1284483 (INB. XRFF	AB004818	90.
periation	os nuclear receptor supramiry 2, group r., i ALSS4245	1.98
(QAAQ95) anatein	ABU46840	. 98
period homotoo 3 (Prescribia)	A6023170	1.98
carborypepidase B1 (tissue)	\$000C7	86.1
(QAA175) protein	1/91/07/10	9.30
hypothetical protein M6(3101	Abostose	8.
ICLAN 1096 protein	A40220A4	26.1
diversionie 6 open raading frame 32	75995744	86.
flavin containing monoozygenase 2	F0570078	0
putative hymphocyte 60/61 switch gene	PERSONAL PROPERTY	0.0
action related protein 2/3 complex, subunit 18 (41 kD)		6.5
96:8C05507.1 /0EF=Homo sapiens, Similar to histamine N-methyltransferase, clone HGC:14500, mRNA, complete cds. //FEA=mRNA /PROD=Similar to histamine N-methyltransferase //DR		6
głyczphorin A (includes MN blood graup)		6
hypothetical protein FLI20700	2E6210 KN	161
Consensus includes gb./MO24561.1 /DEF =Homo sepiens cDNA: FU20908 fs., clone ADSE00417. /FEA=mRNA /DB./XREF=gi:10436870 /UG=Hs.306689 Homo sepiens cDNA: FU20908 fs., AXIQ24561	16689 Homo sapiens cDNA: FLJ20908 fis, 4 AK024561	1.97
addingto delydrogenase I lamly, member A2	NM_003888	1.97
COMPANIES MONOS 90-XV 14513 / PCA=E31 / DB XAEF = 9:11006656 / DB XREF = 51:XV 145135 / CLONE=HEMBA1003989 / UG=Hs. 274266 Homo sapiens cDNA FLI10175 fis, clone HEMBA ALI145135	sapiens CDNA FU10175 fis, clone HEMBA AU145135	1.97
(Javi) 2 exturis C (Javi)	570004	1.97
25 (27) House block and an analysis	NM_024583	1.97
Portable desired Charles, Sharrelated subtamily, member 2	NM_012281	1.97
inflormation provided the control of	AK025430	1.97
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Comments included the first of	GE:3509783} /DB_XREF=gi:13278737 /L 8C004145	1.97
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AND THE STATE OF T	sapiens mRNA; cDNA DKFZp5648222 (fr. AW025579	1.97
Children from the force than the force of th	NM_006467	1.97
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The second of th	A673812	1.97
MARKARY MICHAELS 1/10 CAN TRACES / 1/10 CAN TRAC	sapiens cDNA FU12105 fis, clone HEMBB AU147200	1.97
MANAGED SOCIETY	4U145019	1.97
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Proportional protein FU23188	N52532	8.
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orthon but 614	E99900 HN	8.

Conservation includes giz. M. U. M. D. C. Following supiers in M. W. (1) W. D. C. Z. S.	apiens mt AL080106 U43279 AWZ69335	8 8 8 8
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stobelial differentistion, typophosphation acid 6-protein-coupled receptor, 2 aea, Casa V, type 10X nomine cuticae A blosses and mab 3 related transcription factor 1 customal biogenesis factor 11A	AW269335	2 2
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	AL360141	5.
chemotine (CA3-C) receptor 1	020350	1.5
nactivation escape 2	AW003516	5.
collagen, type VIII, sipha i	8E877796	5
phosphoribosy prophosphate synthetase 2	NM 002765	5.
onsensus includes op.AW970564 /FEA=EST /08   XREF = a: 8160429 /08   XREF = est: EST382665 /116 = Hs. 291033 EST.	AW970584	5
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conservate includes gb.A.117630.1 /DEF = Homo supriens mANA. CDNA DNE2p434D115 (from clone DNE2p434D115). FEA=mRNA /DB. XREF = qr:5912213 /UG=Hs, 252723 inbasomal protein AL 117630	al proteir AL 117630	1.95
hematopoietic PBX-interacting protein	NM 020524	6.
hypothetical protein WG(12262	96250038	1.95
RIAK1009 protein	NM_014895	1.95
acidabes stress induced like	046752	6.1
IRCAL associated protein	AL042733	1.95
KAB31, member RAS ancagene famity	BE789881	1.95
gamma-aninobutyris acid (GABA) receptor, the 1	NM_002042	1.95
hypothetical protein MGC4655	80004908	1,95
entagin-binding sudoprotein (bone staloprotein, bone staloprotein II)	NM_004967	1.95
hypothecial private I US12	NM_018121	1.95
rypoued protein 10,000	MM_018333	26.
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hypothetical protein FU10648	AL049394	- 5
branschétón elongation factor 8 (Still), potypopide 2 (1880, elongin 8)	AC004493	2
neurofilament 3 (150kg nedum)	NM: 005382	3
estrogen receptor 2 (ER beta)	AF060555	26.
mentarane-spanning e-domains, subfamity A member 2 (fo fragment of 195, high affinity I, receptor for, beta pohypeptide)	NM_000139	- 2
offactory receptor, family 1, subfamily 6, member 1	NM_003555	1.94
COTSON TO STATE OF THE STATE OF	1509 f AX021571	9
Syraca hormone receptor interactor 10	NM_004240	1.94
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CAPONE ANY OTISE A	A6016195	*
prion protein (p27-30) ((routzfeld-lakob disease, Gerstmann-Strausler-Scheinker syndrome, (atal familial insomnia)	NH_000311	<b>3</b> .
II insurance	NH_003490	1.93
spart/bateonectin, cwcv and kazal-like domains proteoglycan (lestican)	AF231124	1.93
mucin and catherin-like	NH_017717	1.93
zink finoar protein 42 (Inveloid-spacific retribok acid-responsive)	M58297	1.93
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and the place of the second	80000 H	9 9
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guaraine nucleobbe binding protein (6 protein). Alpha 11 (6q class)	A1040021	
entagrin, alpha M (complement component receptor 3, alpha; also known as (011b (p170), macrophage antigen alpha polypeptide)	NH_000632	1.93
heat shock 70kD protein 1.A	NM_005345	1.93
afkaine phosphetze, intestinal	NM_001631	1.93
synapticianin 1	NN 003895	1.93
AMD, I contain	AKOO1538	- 63
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human epistopima-specific 3 alpha	NM_006683	1.93
ofgodendracyte innege transcription factor 2	A757419	1.93
chromosome 2 open reading frame 3	8(000853	1.93
metria metallogordeinase 7 (matriksia, uterine)	KM 002423	1.93
National State of the State of	MM 014937	3
The state of the s	19510-14	3
(NU), income against oecupentapregic nomolog 3 (Urosopnita)	A-010601	1.93
standardisc process	NM_014357	.93
hypothetical protein PR01496	NH_018603	1.92
transmenterme 6 superfamily member 2	AX024515	1.92
protocuparin alpha 9	NM 014005	1.92
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Compensus includes gb:AL121981 /DEF=Human DNA sequence from clone RPS-1061(18 on chromosome 1p36, 22-36, 33. Contains ESTs, 5TSs, 6SSs and e Cp6 island. Contains the 5 par	t of AL121981	1.92
dopartine receptor 03	1,20469	1.92
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cytochrome P450, subfamily IIIA (nightedipine azidase), palypeptide 4	NM_017460	1.91
hypothetical protein FU10430	NM 018092	1.91
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cytochrone P450, subfamily XI8 (steroid 11-beta-hydroxylase), polypeptide 2	XS4741	1.91
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Consensus includes gb.M022408.1 (DEF =Homo sepiens cDNA FLJ12346 fis, clone HAMMA1002297, highly similar to Homo sepiens mRNA for Rab6 GTP-ase activating protein. FEL=mRNA M0022408	e activating protein. /FEA=mRNA AK022408	
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MASS. member AS encourage training	AF267863	
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ytochrone P4So, subfamily IX (mephenytoin 4-hydroxytaxe), pohypeptide 9	AV646536	
Consensus includes gb.W570199 FEA=EST (08_XRFF=g.4533573 /08_XRFF=estto76607.s1 /CLONE=INA(E:2184181 /UG=Hs.182183 Homo sapiens mRNA for caldesmon, 3 UTR	nRNA for caldesmon, 3 UTR AUS70199	
call division cycle 258	AL109804	
SRY (sea determining region 1)-bas 11	AW157202	
GAADS99 protein	\$6004598	
integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen (D418)	NM_000419	1.83
hypothetical protein FLI 10044	017980	
hypothetical protein FU13605	NH_024577	<b>3</b> .
Consensus includes go:8F222916 /FEA=EST /DB_XREF=gi:11130093 /DB_XREF=gi:7q25a04.x1 /CLONE=IMAGE:3699342 /UG=Hs.331207 ESTs	8,5222916	
Lansansus includes gb.A.121582 /DEF=Human DNA sequence from Gone RP11-28009 on chromosome 20. Contains an RMF11 (ring finge protein 11) (SID1669) pseudogene, ESTs, STSs - A.121582	D1669} pseudogene, ESTs, STSs . AL121582	
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omsensus includes go.AW973834 /FEA=EST /OB_XREF=gi:8165022 /OB_XREF=est:EST385936 /UG=Hs,105684 ESTs	AW973834	
onsensus includes go.MC00244.1 /DEF=Homo sapiens CDPA FLI20237 fs. clone COLF5879, highly similar to AB023230 Homo sapiens mRNA for KIAA10	3 protein. /FEA=mRNA /DB_XRE AX000244	
NH_00172 builtous perrephysical antigen 1 (73-07-4-01.0)	NM_001723	
nomodomini, tetti-specifik	NH_001726	
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proteasome (prosome, macropain) subunit, beta type, 2	80000268	1.63
hypotherical protein FU11871	NM_025117	1.83
6-substrate	NM_006658	1.83
Consensus includes gb.MC23798. 1 / DEF = Homo supiens CDNA FU13736 fs., clone PLACE3000156. FEA=mRNA /DB.XREF=gi:10435842 / AG=Hs.31532 Homo supiens mRNA. CBNA DKF2p AK023798	KFZp AK023798	1.83
hypothetical protein FU11637	NM_024967	1.83
DMA-dependent protein binese catalytic subunit-interacting protein 2	A478592	1.83
endomucin-2	NM_016242	1.63
dystrobrevin, alpha	U26744	1.83
Shipdianshipytamine (serationin) receptor 7 (ademylate cyclase-coupled)	NM_019859	1.82
CONTRACT (ACCUSE)	NM_005076	1.82
The first of the f	NM_012104	29.1
remains regarded acquisition of the property of group or member c.	MA_006185	7.5
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6/07-2 for gonadotropin inducible transcription repressor-2	NM_016264	28.
othactory receptor, tently 7, substantly A, member 17	AC005255	28
visual system homeobox 1 homolog, CMX10-like (zebrafish)	NM_014588	3.1
ademydde cydasa 2 (brain)	A8028983	28.
KDA1031 protein	NM_025013	1.82
CONSOURD INCLUDES GO MESSI 93 /FEA-EST / DB_XREF = 91:4970533 //DB_XREF = est: w408/102.r1 / KLONE=IHA6E:2336763 / UG=HS. 247551 metazin 1	A693193	1.82
solvine carrier family 11 (proton-coupled divalent metal ion transporters), member 1	050402	1.82
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Impotencia protein [122297	NM 025135	2
nuclear receptor subhamity 0, group 8, member 2	NM_021969	1.82
litary ortholog of mouse early 8-cel factor 2	NM_022659	1.62
Pypodhetical protein FU11336	NM_018393	1.82
of RC - while despite your center.	NM_006613	1.82
Institute devent state (st. g. 1815-1816) and characteristics of properties of the state of the	AM_016412	29.5
hypothetical protein FU14117	NM 022777	8 2
CASP8 and FADD-like apoptoria regulator	AF009616	3,
KIANG680 game product	AW295193	1.82
hypothetical protein FU10034	NM_017973	3.1
Lamor necrosis factor (figure) superfamily, member 15	NM_005118	1.82
hypothecial present 12/1269	NM_025107	3.
og men innexes of its innexes is a constant of the control of mendom t	NM_0220/3	3
potassism invasiva external subtantiv I member 9	NA ODA983	28.7
sodium channel, withage-gleed, type IV, alpha polypetride	NM_000334	3
hypothetical protein FU14084	NN_021637	28.1
Lin-70 protein; filially ortholog of mouse LIN-78; mammalian LIN-7 protein 2	NM_022165	1.82
Machine respect reserving protein	A/203397	1.82
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chemotine (C.4 motif) receptor 5	NH 000579	¥ =
fibronects leurine into transmembrane protein 3	NM_013281	1.8.1
ampidensia receptor 2	NM_000686	-6.
PRO0039 protein	NH_014113	1.81
phosphomosidae-1-kinase, regulationy subunit, polypeptide 1 (p55 alpha)	A1934473	1.81
machighicen mass, beta (300L)	A8018261	1.8.1
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setting contents inhibitor clade 8 (ovaluation) nember 10	MA COSON	
cyclic mucheolide gated channel beta i	U18945	<u>.</u>
acetytholinesterase (TT blood group)	MS5040	1.8.1
optobine mespion-like factor 3	NM_015986	1,8,1
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wersus includes gb.MQ23891.1 /DEF=Homo supiens cDNA FU13829 fs, clone THYR01000625. /FEA=mRNA /DB_,RREF=gj:10435964 /UG=Hs.28 a confragration of protein 1 Told protein 1 T	500 Homo sapiens cDNA FLI13829 fi AK023891
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rulabe prostate and a transfer and a	AU158251
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myeloid/ymphoid or mised-lineage keukemia (trithoras homolog, Drosophila); translocated to, 4	A8016898
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cyticin, basic protein of sperm head cytoskaleton 1	222780
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Consensus includes gb.M.137063 70EF=Human DNA sequence from clone RP1-104L14 on chromosome 6 Contains part of the AXAP7 (A kinase (PRKA) anchor protein 7) gene, ESIs, 5TSs a A.137063	ichor protein 7) gene, ESTs, STSs & AL137063
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rycain K	
nsulin-Else growth factor binding protein 2 (36kD)	NM_000597
one cut domain, family member 1	U96173
Calpain 6	NM 014289
hormonally uprogulated Neu-associated kinase	NM_014586
utracin	AL 132773
QAN 264 protein	A8040812
phosphate cyclophitransferase 1, choline, beta isotom	NM_004845
UM0961 protein	KM_014898
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COTOMINATION OF SECTION OF THE FIRST CONV. FLIZZ392 fin, clone HR107868. FEA=mRNA (OB_XREF=9:10438761 /UG=Hs.275464 Homo supiens cONA. FLIZZ392 fin, clone HR107868. FEA=mRNA (OB_XREF=9:10438761 /UG=Hs.275464 Homo supiens cONA. FLIZZ392 fin, clone HR107868	mo sapiens cONA: FU22392 fis, cl AX026045

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DNE=IMAGE:22392 /UG=Hs,13223 Hamo sapiens mBNA hull length insert CDNA clone EUROI FEA=mBNA /DB_,XREF=gi:10438467 /UG=Hs,287692 Hamo sapiens CDNA FU12365 fs, clone MANIM ////////////////////////////////////	ate decarbonylase 1 (brain, 67kD)	NM_013445
DNE=IMAGE:22392 /UG=Hs,13223 Homo sapiens mRNA full length insert CDNA clone EUROI FEA=mRNA /DB_XREF=gi:10438467 /UG=Hs,287692 Homo sapiens CDNA: FU22180 fs, c KLONE=MAMMA1002392 /UG=Hs,302075 Homo sapiens CDNA FU12365 fs, clone MAMM	phon factor ets	AF147782
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//LONE=HAMMAI002392/U/G=Hs.302075 Homo sepiens cDNA FU12365 fs, clone MAMM	al membrane protein 1	NH_001423
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6.1 / OEF = Homo supiens + OHA FUL 2624 fis, clone NT2RH 4001754, / FEA=mRNA / OB - XREF = 0; 10434225 / UG=H1, 306639 Homo supiens + CDNA FUL 12624 fi	
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Consensus includes go.AL36504 (DEF = Numan DNA sequence from clone RP1-14N1 on chromosome 1q21-1-21.3 (ontains ESTs, GSSs and STSs. Contains the FLG gene for profilaggin and AL356504	

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/g-whole	AW006438	1.7
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hypothetical protain PR02268	NM_018520	1.7
hypothetical protein FU13942	NM_024581	1.7
gycine neceptor, alpha 3	NH_006529	1,7
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Commensa includes ab AW 405975 FEA = EST 708 XRES = a; 692 5032 708 XRES = est ULHF 810 - acc + -05-0-ULH T (CONFE HAGE: 1060368 AUG = Hs. 247721 Home stations clone mcs51-54 i AW 405975	AW405975	1.71
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Consensus includes gb.16'055011.1 (DEF =Home sepiens clone 24'58) mRNA sequence. /FBA=mRNA /DB_XREF=gi:3005734 /UG=Hs.137173 Home sepiens clone 24'587 mRNA sequence	AF055011	1.7
Consensus includes gb.MU158606 /FEA=EST / 708_XREF = gi-11020127 / 708_XREF = est-XM158606 / (LONE=PLACE300406 / UG=Ns.287636 Homo supiens cDNA FU14319 fis, clone PLACE31 AU158606	( VI) 158606	1.7
Conservas includes do ALOSO086.1 OFF #Home sapiens mRNA: CDAA DIGZOS6411762 (from clone DIGZOS6411762). FEA=mRNA ///38 XREF=a; 526.5502 AUG=Hs. 274538 Home sapiens n ALOSO086	AL030086	1.71
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Land protein	NN_014462	2.7
A supple mannosidase K	NM_020379	1.76
pre-mIMA processing factor 31 homolog (yeast)	A334332	1.76
Consensus includes gb-MO22233.1 / DEF = Homo supiens CDNA FU12173 fs, clone MAMMA1000696. /F.EA=mRNA /DB_XREF=gi:10433588 /US=Hs.306630 Homo supiens cDNA FU12173 1 M022235	AK022235	1.76
protocacherin beta 11	NM_018931	1.76
T-cell leadenis/yrphone 6	NM_012468	1.76
capain 5	NM_004055	1.76
Commensus includes gb-MASS 5096 /FEL=EST / DB_XREF = gi-232 5635 / DB_XREF = estinit 40e-01.s.1 / (CLONE=1MAGE:994968 / AIG=14s.26295 Homo supiens mRNV, cDNA DKF 2p.5860 1122 (from MASS 5096	AA555096	1.76
solute carrier tanity 6 (neurotransmitter transporter, creatine), member 8	AW276522	1.76
lethel (3) malignant train tumor ((3) mbt protein (Drosophita) homolog	AW445040	1.76
UV-8 repressed sequence, KUR 7	BE148534	1.76
postmeiotik segregation increased 2-like 6	038503	1.76
sárbain sálent mating type information regulation 2 homolog 2 (5, cerevisiae)	A090841	1.76
probes tyrosine phosphalase, non-exceptor type substrate 1	AL049634	1.76
ymphome variant translocation 1	NH_002035	1.76
	NH_012334	1.76
	NH_005797	1.76
ubiquitin-conjugating enzyme E2 veriant 2	AL031291	1.76
gh344_108534.1 /DEF=Homo sepiens hypothetical pratein PR02893], mRNA, /FEA=mRNA /GEH=PR02893 /PR00=hypothetical pratein PR02893 /DB_XREF=gi:8524214 /UG= Hy_018634	NM_018634	1.76
Consensus includes go.18/968134 /FEA=EST /DB_XXEF=9:12335349 /DB_XXEF=est:60226912181 /CLONE=IMAGE:4357349 /UG=Hs. 250723 FX506 binding protein 12-rapumycin associa	8F968134	1.76
	AL137716	1.76
proteinas ) (serine proteinase, neutrophil, Wegener granufonatosis autoantigen)	HM_002777	1.76
Apiens PROZEG7 mRNA, complete cds. FEN=mRNA /PROD=PROZEG7 /OB_XREF=9:7770214 /NG=Hs.321170 Homo sapiens PROZEG7 mRNA, complete cds /	AF119889	1.76
	A8004903	9.7
	KM_024021	-7 <sub>6</sub>
Consensus includes go.XM974995 /FEA=EST /DB_XREF=gr.8166198 /OB_XREF=est:EST387100 /UG=Hs.292787 ESTs	AW974995	1.76

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U41163	97.1
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Compansus includes go. N.025180. I VEF = Homo sapiens cDNA: FLIZ1527 fis, clone (OLO596). IFCA=mRNA (DB_XREF=gi:10437643 /UG=H1.306779 Homo sapiens cDNA: FLIZ1527 fis, cl ANO25180	1.76
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inhibin, beta 8 (active AB beta polypeptide)		7
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pipecolic acid oxidase		7.
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coagulation factor II (thrombin) receptor-like 1	NH_005242 1.	7
IDAA6275 gene product	NN_014648 1.	Σ.
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offschor vacedo: family 10, subfamily H, member 3	38	7.
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hypothetical protein (U10209	9	7.
6W-associated hyroaine phosphoprotein p62 (Sam68)		
hypothetical protein FU10488		z
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hypothetical protein FU22601	NM_024822	<u>.</u>
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inside. Bit growth tartor binding protein, acid labite subunit	AW338791	1.74
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Consensus includes gb.A1275371 /DEF=Homo supiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, clone 16 /FEA=(DS /DB_XREF=gir)573002 /UG=Hs.272356 Ho A1275371	4o AI275371	1.74
Consensus includes gix. VB2306.1 /DEF = Homo supiers unknown protein mRWL partial cds. /FEA=mRNA /PR0D=unknown /DB_XREF=g:1938333 /UG=18.123081 Homo supiers unknown g UB2306	1 082306	1,74
poliowins receptor-related 2 (herpenins entry modator 8)	NM_002856	1.73
U3424 Bubblis dapb, jajf, jajf genes corresponding to nucleotides 1358-3197 of 138424 (+5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	138424	1.73
four and a half LIM domains 1	AF220153	E. 1
FEBB 1 family member in MIC data I region	NM_005844	3 5
Proposed premi Full USS	MA 020803	2 2
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described branches (Created) branches 5	AB011155	2
Consensus includes ab: RC05092.1 (DEF=Home statiens, clone IMAGE:3843012, mRNA, partial cds. //EA=mRNA PR00=Unknown (protein for IMAGE:3843012) //38 //ABE=ai:13477248 // BC005092	A 80005092	5.7
40-4116715.1 / DEF #Wome septems PR02829 mRNA, complete cds. / FEA=mRNA / PR00=PR02829 //DB_JXREF=qi.7959928 //JB=Hs.256256 Home septems PR02829 mRNA, complete cds / MF116715	1/ AF116715	1.73
collagen, type I, alpha I	NM_000088	5.7
golgi eutoantigen, golgin subtamily b, macrogolgin (with transmembrane signal), 1	N53479	1.73
secreted protein of unknown function	BF 440021	2.
700618 protein	NN_014133	5
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potasium immardy-recitifring channel, subfamily I, member 5	147208	1.73
microsonal NUC+-dependent retinal deby/dragenase 4	AF086735	1.73
solds carier lamity 30 (zinc transporter), member 4	NM_013309	1.73
UAL2, member IAS oncogene family	AW301641	1.73
matti metaloproteinase 16 (membrane-inserted)	NM_022564	1.73
carbonypepbidses, witelogenic file	NM_031311	2 :
and known protein 14 (done pit_44)	NM_003441	<u> </u>
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defect in black case from some confidence of the	NH 014618	: =
ipase protein	80001698	2
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hypothetical protein FU20337	AL096712	2
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Conference of the conference o	MH_U1/422	2 5
RAMONS protein	A/122905	2
solvte caries tamity 26, member 3	NH 000111	2
Commenses includes go-MO17721 /FEL=EST /OB_UREF = gi: 479910 /OB_UREF = ett: e3911:s1 /CLONE=IMAGE: 361389 /OG=Hs. 49117 Homes septems mRNA: cDNA DNZ 2p564H1662 (Hom	m AA017721	1.73
are regenerating talet derived like, human homolog (pencreatic stone protein-like, pancreatic thread protein-like)	NH_006508	2
XXI (sectomming region 1)-box 9 (surpometix dysplasts, autosomal secretisal) Bus to to contract of the contrac	NH_000346	2
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hypothetical protein FU13166	NH_025003	1.7
Communic includes gb.AW149844 /FEA=EST /DB_XREF=gi.6197740 /DB_XREF=est=142.010.1 /CLONE=IMAGE-82620771 /LIG=His.167140 ESTs, Moderately similar to CING_HUMAN YOLTHA WW149844	A AW149844	1.73
cyclin-dependent binase 6	Al738463	1,73
Nearthad hizzbed-related protein 5	MM_003015	7

Epstein-bar wirs induced gene 2 (tymphacyte-specific G protein-coupled receptor)	NH 004951	2
hypothetical protein FU11561		2
hypatherical protein FU20637		2
tumar necrosis Incta, alpha-induced protein 6	NH 007115	2
Compensus includes gb.2W691491 /FEA=EST /08_	AV691491	: 5
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sphingosine : -phosphate iyase 1	=	2
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uncharacterized hypothalamus protein HT011		~
Consensua includes 95-XX002179.1 /DEF = Homo sepiens cDNA FU11317 fs, clone PLACE1010261, moderately similar to SEGREGATION DISTORTER PROTEIN. FELX=mRNA /DB , XREF = gi:70   XX002179	AX002179 1.72	~
ertagrin, beta 8		~
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hypothetical protein FU20069	AL080179 1.72	
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Consensus includes gb-AL133018.1 (DEF = Homo septions mRNA; CDNA DNFZp434f0327) (from clone DNFZp434f0327). If Eb = mRNA /DB XBEF = oi; 6453498 /Ms=Hs 70527 Homo senions		
decreasons 11 open rating frams 8	3	
hypothetical protein d/79617.1	NH 025225	
Laste mergica, type 2, member 8		
b)A33532 (DEF = Human DNA sequence from clone RP11-487F5 on chromosome 6 Contains the 3 part of the GRIK2 (glutamate receptor, ionotropic, kainate 2) gene,		
Drintoming growth Lactor, beta 2	5F061658 1.72	
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foroblast activation protein, alpha	
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collagen, type VI, alpha I	M20776	
signal transducer and activator of transcription 2, 1133.0	581491	1.71
\$\text{phyK}\$13051.1 DEF = Home sepiens close FLB3535 PR00858 #RNA, complete cds. \(\text{F} \text{C} = \text{mRNA}\\ \text{PR00} = \text{PR00858}\\ \text{DB}\\ \text{ARE} = \text{gir}\$11493408 \(\text{AB}\\ \text{C} = \text{AB}\\ \text{C} = \text{C}\\ \text{C} = \text{C}\\ \text{C} = \text{C}\\ \text{C}\\ \text{C} = \text{C}\\ \text	S AF1300S1	-
Conservation includes 90-AL 136179 (OEF arrhuman DNA sequence from clone RP3-32214 on chromosome 6. Contains the SOX4 gene for SRY (see determining region Y)-box 4, a pseudogene a AL136179	y AL136179	1.71
KAMOSS protein	AB011129	1.71
tumor stroms and activated macrophage protein DLM-1	NM_030776	17.1
ICLAN 1000 protein	BF062942	1.71
tumon necrosis lactor (figand) superfamily, member 13	AF114013	1.71
יושל משקיים ולבלי	NM_005576	1.71
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retrinoir acid repressible protein		1.70
hypothetical protein FLI14075	NM_024894	1.70
cambre O-ccanopitransferase	NM_021151	1.70
SUTTICATION PRODUCTION BETWEEN THE SUTTICATION OF T	192201	1.70
Towns hairs, cell'-dependent, type II	NH_006259	1.70
The Control of the Co	NM_014020	1.70
carrier ordinates	A8051441	2.5
Conservate includes gb.A.161956. I DEF=None supers mRNA, cDNA DNZ2p361A1712) (from clone DNZ2p361A1712). FEA=mRNA /DB 2REF=ai:732B008 A1G=Hs 306492 Home susies		0,7
potassium channel, sublamily K. member 7		1.70
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6 protein-couped merchan 86	NH_023914	1.70
Danaporte, A. Al'-banda cassette, sub-family 8 (MDR/IA)	NM_018833	1.70
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reprovided programmes and programmes	AF250321	1.70
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injourned press (L2393)	NM_024643	1.70
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hemoglobin, alpha 2	150399	2 2
catarian (cachenin-associated protein), alpha pseudogene 1	237994	1.70
transient neceptor potential channol 6	NM 004621	1.70
Myodhekial protein D/G 1,0101823	AX026105	02.1

×	octobe carier family 3 (systims, dibasic and neutral annino acid transporters, activator of cystins, dibasic and neutral annino acid transport), member 1	NM_000341	1.70
-	SWAT MICK I associated repressor protein	ALS2 4033	1.70
Æ	rypothetical protein M6(3020	NH_024048	1.70
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Ε,	macophage stimulating I receitor (c-met-related hyrosine kinase)	NM_002447	1.70
3 3	DESTRUCTION OF THE PROPERTY OF	A911273	1.70
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3	CONSIGNED STATE ACCOUNTS 1. 10 FF = Howns septens mRNV: CDNA DIG 2586[111] (from clone DIG 2586[111]. IF EA=mRNA /DB_XREF=g: 5262726 /UG=H: 326580 Homs septens mR ALD80233	nf AL080233	1.70
ā	bunor necrosis factor (ligand) superfamily, member 13	AF114012	5.7
6	chalmephasphotransferase 1	AF195624	1.70
Œ.	interferon regulatory factor 2	NM 002199	1.70
2	Abinding motif, single stranded interacting protein 2	AA536000	1.70
3	Consensus includes abAY700891 FEA=EST // IB XIRE=a:10302862 //// B XIRE=c:10302862 /// B = 6KKB0D03 A IG=H+ 292477 FSTs	47700891	
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	sustantive immunoclebulish merester subtamin & festivant TM domain), member 4	AE041361	2.5
	the factor and the second seco	107100	2 !
12	TT INC. INC.	WA_013539	0.5
5 1	using the state of	XX 10 XX	1.69
È.	Typosocia professional (10.81)	AX022786	1.69
Ē.	hypothetical protein FU12121	NM_024978	1.69
9	COMBONIUS INCLUDES DE DE LA STATE DE LA STATE DE LA STATE LESTAN 147962 ALLONE = NAMINA 1002250 /UG=14, 301509 Homo supiens CDNA FLI 12339 fs., clone MANN AU147962	M AU147962	1.69
2	other cell lectin-blu receptor subtrarity 0, member 1	030610	1.69
E.	protectifycan 1, secretory granule	MM_002727	69'1
5.	growth factor independent 1	NH_005263	1.69
3	Consensus Includes gb-IL033538 / DEF = Human DNA sequence from clone RP3-477H23 on chromosome 22q12.1-12.2 Contains parts of one or two novel genes, ESTs, STSs and GSSs /FEA= IL033538	= AL033538	1.69
3	calsequestrin 2 (cardiac muscle)	NM_001232	1.69
ğ	Consensus includes gb:AL13743.1 /DEF=Homo supiens mRNV. cDNA DNF2p434L092 (from clone DNF2p434L092). /FEA=mRNA /DB_XREF=qi:680795) /UE=Hs.306457 Homo supiens mA	A AL 137403	1.69
3	keratocen	NM 007035	69'1
ā	putable perazisone microbody protein 175.1	NM 015887	1.69
. <u>E</u>	Einwess homolog (Drosophila)	AX000721	1.69
F	MPeas, $H+M+$ eschanging, bets pohypopride	NH_000705	1.69
æ	jegran syndrome antigen 8 (autoantigen La)	62628359	1.69
Š	Consensus includes go: ALOSOOGS. 1 DEF = Homo sepiens mRNA; CDNA DKF2p5641062 (from clone DKF2p5641062). FEA=mRNA /DB_XREF=gi:5262475 /UG=Ns.272534 Homo sepiens mR1	11 AL080068	1.69
₫	KDAM934 protein	AW134976	1.69
£.	protein tyrosine phosphatase, receptor type, 0	NM 002839	1.69
£	hypothetical protein FU10178	AK001040	1.69
₩.	HE file Protein	NM_020356	1.69
I	met proto-oncogene (hepatocyte growth factor receptor)	8E870509	1.69
Ē	I Inducible cytodiane A2 (manacyte chemotactic protein 1)	\$69738	1.69
Ē	transcription elenquiton factor (SIII) elengin A2	NH_016427	1.69
5.	Consensus modes go. HOQ 2203. I NEF = Nome septens hameobox protein Og 1 2 (OG L 12) mRNA, partial cds. IF EA = mRNA (EEN = OG L 12 / PROD = hameobox protein Og 1 2 (OB _ XREF = gi. 297		1.69
Ē.	mmanoglobulan larinda locus	x93006	1,69
	Transportate tipopoptial process (144	NM_022915	1.69
7 6	and an entire or primoria vira oncogene homolog 3 (protein binase 8; gamma)	NH_005465	69.1
1. 1	month of the first the fir	AF352026	69:1
	newwork is printed to the control of	M 001562	69.1
9 5	e green taken keupen (i int nor i b) associated protein i	NM_014380	69.1
ž	An insurence security, immunoser to	NM_003532	69.
\$ \$	in the property of the propert	AL35379	69.
F .	DESCRIPTION OF THE PROPERTY OF	NH_024729	1.69
5	Comments include the ALL 17659 INFERENCE CONTINUE AND INFERENCES A	AX025619	1.69
Ē	GOOD STATES CONTROL OF THE CONTROL O	VI 0063EC	6.5
8	acide protein 1	NM 018058	6.
1	eitogen-activated protein kinase 8	U34822	69:1
Š	J. (1-3 Th' protein	AC003007	1.69

Copplain resistance-associated overcons sed protein	AW089673	1.69
CONSTRUCTOR SHOULD SHOW SHOWN	8 f AK022120	1.69
The second second of the secon	5//154	69.1
monthis, beta 10	AF090913	91
oodkom channel, vorkage-gated. type XII, alpha podypestide	AF150882	9.1
manipuncy-exposited protein	AF041410	9.
(USS amogan (gp6))	NM_001772	9.1
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Zanazari-seration protein 2.	41979087	9 9
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atrial, atrial		9
bactine rich repast (in FUI) interacting protein 1	AF130054	1.69
offactory receptor, tarrily 5, subharrily V member 1	NM_030876	1.6
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enche-nich, diems inschrätel 1	WW 005097	69.
IJA0346 protein	AA521267	6 9
(0.0523)	AX026768	1.69
IGMA1053 protein	AL117523	1.69
MCOSO43.1 /DEF = Home supiens, Smilar to tumor necrosis factor receptor superfamily, member 10s, decoy without an intracellular domain, clone MGC:12787, mRNA, complete cds.	E BC005043	1.68
COMBANIAN INTO AND	Tot AW663632	2.
Modew Progres A mental retardation protein interacting protein I	AWS93143	3
news as y protein. The stricted follows from I recented throughout the section?	A5011095 M98200	39.
VAMP responsive element binding protein (	NM 004379	8 9
docking protein 2, 560	A1828929	1.68
Vruppal-Bas factor 4 (gut)	NM_004235	29.
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THE	ALISZU/4	99.
DETA 41420 arrein	ALORO148	8 5
VV-4 repressed sequence, HUR 7	RF148534	8 5
optochrome P450, subfamily ( (aromatic compound-inducible), polypeetide 2	NM Ono761	9 5
SAY (sea determining region 1)-box 20	AB025355	3
Oustair Incl. ALOSO166:Homa sepiens mRNV; cDNA DNF2p58601122 (from clone DNF2p58601122) /cds=UNXNONIN /gb=2LOS0166 /gi=4884381 /ug=Hs. 26295 /len=2654	AL050166	1.6
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dodd/ymphoid or mised-lineage leutemis (inthorax homolog, Drosophila); translocated to, 2	AA715041	2 5
gletamets-emonia ligase (gletamine synthase)	008626	3 29
ght.1448.1 /DEF=Human ig rearranged kappa-chain gene V-I-region, complete cds. /FEA=mRNA /DB_XREF=gi:398492 /FL=gb:114458.1	114458	1.68
hypothetical protein FLI21302	NM_022901	1.68
CONTRIBUTED INCLUDES DELIVERAL CHURAN CHROMOSOME 16 BAL CLORE (11987) SK.A. 38804 /FEA=MRNA /OB_XREF=gi:3417290 /UG=Hs.177961 Human Chromosome 16 BAL Clone (11987) U95737	7 1 1 1 1 5 7 3 7	<u>-</u>
NETWORK (A. MOUT) PRESIDENT S NETWORK (A. MOUT) PRESIDENT S	NM_001837	33
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hepatocyte nuclear factor 4, gamma	NM 004133	2
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octassium voltage-gated channel, KGT-like subhamity, member 4		
	NM_004700	1.68

	protuglandin Freespar (FP)	NM_000959	3.
	HI historie family, member 4	NM_005321	1.68
	negibor of Atlanes enclosing protein 95	AB015332	1.68
	source Larrar ramy 2 (hourteen glucose transporter), member 10	7470EO NN	3
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	Symptopical formal framework for the symptomic formal form	NM_007286	99.
	includes bettief about data to the contract of	MM_0044/3	2 3
	options (survividos): famish tree	AC004832	9.
	sprindin-file	AF156153	8 5
	Consensus includes go.XXX24568.1 /DEF=Homo supiens cDNA: FU20915 fis, clone ADSE00692. /FEA=mRNA /DB_XREF=gi:10436878 /UG=Hs. 306691 Homo supiens cDNA: FU20915 fis, xXX24588	AX024568	3
	Conservation of MG 190579.1 (DEF Homo supiens clone 24487 mRNA sequence. If EA=mRNA /DB_XREF = gi.3387951 /MG=Hs.283819 Homo supiens clone 24487 mRNA sequence	AF070579	39.
	surfacture pulmonary-associated protein 0	NM_003019	1.68
	boson family member 5.	NH_004984	1.68
	Production of the Control of the Con	NM_018301	.68
	AT zee, emmorphosopholipid treasporter-like, Class I. type 8A member 2	NA_016260	2 5
	stablein	NM OO3154	è :
	Consensus includes go. 15 ES83744 FEA=EST DB_XREF=gi:10345354 DB_XREF=et:501513656F   TCLORE=IMAGE:3915133 ALG=HL:169274 ES1s, Highly similar to IFT2. HUMAN INTERESTANCE	BE888744	(9)
	cytadrome P4S0, subfamily IIA (phenobarbital inducible), polypeptide 6	T67741	1.67
	Consensus includes gio.XXQ21930.1 (DEF = Homa supiens cDNA FUL11868 fs., clone HEMBA1006993. /F.EA.=mRNA /DB_XREF = gi:10433231 /UG= Hs.302260 Homa supiens cDNA FUL11868 fs. AXQ21930	AK021930	1.67
	parent-centred grown factors respect along polypoptide	H22734	1.67
	TWO promotes in the common of	NM_005750	19.
	Depomesin I (alpha)	050479	9.5
	hypothetical protein FU1 4001	M323/0/	9 5
	hyth axidase	BES03425	6 6
	COID artigen, b polypeptide	NM 001764	19
	Typicae bria	NM_003294	1.67
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	Jacob II to e established Orestonia Co A designation and made all contents of the contents of	NH_022001	1.67
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	hy abronoglucosaminidose 4	MM_012269	è 5
		NM 022903	9
		102326	19
	recombining binding protein suppressor of hainess (Drosophila)-like	NM_014276	1.67
	1988.1 /OEF = Hama supiens cDNA FU11926 fs. clane HEMBB1000374. /FEA=mRNA /OB_RRF= gi:10433297 /UG=Hs.306617 Hama supiens cDNA FU11926 f.	AX021988	1.67
		NM_004455	1.67
	Synchronia (No. 1) to the April 19 (artistator / April 19 (artistato	NM_004820	1.67
		NM_005462	1.67
	συρλούλει γγισριστέ	NM_012429	9.5
	Consensus includes gb.W024525.1 /DEF=Homo supiens CDN: FUZ0872 fis, close ADIA/02604. /FEA=mNA /DB_XREF=q:10436827 /UG=Hs.306683 Homo supiens CDN: FUZ0872 fis. , MDF42220	W024525	6 6
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		AF112207	1.67
	commercial and control of the contro	NM_003839	19.
		100100 MM	9 5
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	cytodorom P450, subtrain! III. (niphefespine asidaes), p. phypoptide 3	NM_000776	69
	iomo sapiens CDN. FU23167 fs, clone LN609902. /FEA=mRNA /DB_XREF=gi:10439765 /UG=Hs.287730 Hamo sapiens cDN. FU23167 fs, d.	X026820	1.67
	spores grown included the spores of the spor	KM_001963	1.67
	34446 FEA=EST OB XREF = 412557660 MB XREF = est=17279-01 st M10NF = 1NARE-744216 AIG=H- 1168AD FCT.	AW003022	9.
		NH 001290	à 5
		N421559	.91
	Mary orthodog of mouse ganglookide-induced differentiation-associated-protein 2	NM_017686	1.67
	UD-4-sechi-alph-bogstecommissophepide H-kerhjogladosamin/Pransferse 3 (salkk-13) UD-4-sechi-alph-bogstecommissophepide H-kerhjogladosamin/Pransferse 3 (salkk-13) UD-4-sechi-alph-bogstecommissophepide H-kerhjogladosamin/Pransferse 3 (salkk-13)	NM_004482	1.67
	CONSTRUCTOR DAY SET SET STATE OF THE SET SET SET SET SET SET SET SET SET SE	1049285	1.67
	jamonij homdog (muses)	AA4/96/8 86029530	
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	himme necrosis factor (figured) surrectarily member 10	NN_000905	1.67
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	E3 ubiquitin ligase SAURE2	47014180	9
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	plakophilin 3		9 5
	Consensus includes gb-AL050042.1 /DEF = Homo septiens mRNA: cDNA DIGT265610824 (from done DIGT2556610824). /FEA=mRIN. /DB. XREF = 41:4884284 /UG=1s. 306309 Homo septiens		9 -
	COTHERS INCLIDED SOLAR 47 4615 FELX=EST (08_XKEF=g;7044721 / 08_XKEF=est:xy18x02.11 //LIONE=INAGE:2833506 /UG=Hs.250988 ESTs		191
	phosphohysine phosphohistidine inorganic pyrophosphate phosphatase	NH_022126	1.67
	decolain domain receptor family, member 2	NM_006182	1.67
	Torboad box 22 (MFH-1, mesenthyme forthoad 1)	NM_005251	1.67
	Productive Control of the Control of	105235	1.67
	riperatorises promises and a substance of the substance o	NM_018575	1.67
	cytochrone P450, utdramiy IVF, polyspecide 2	AA805318	<u>.</u>
	Consenses includes go.AW035172 FEA=EST /DB_XREF==5:6040324 /DB_XREF==1x=05609.x1 /KLONE=IMAGE.2605368 /UG=Hs.243366 5513. Highly similar to KPCH HUMAN PROTFIN WROSK172	AW085172	è (
	secreted Mizzled-related protein 4	AW089415	29
	Consensus includes gp. AF 306291.1 / DEF = Home sapiens serologically defined breast cancer antigen NT-8846 mRNA, partial cds. FEA= mRNA, PR00= serologically defined breast cancer a NF308291	AF308291	1.67
	apprent i (chandratin suffite protecylytan 1, large apprenting protecylytan, antigen identified by monoclonal antibody A0122)	NH_013227	1.67
	COMPARTUR MANAGES SES FEMERS TOB ZREF = 91:3182414 FOB ZREF = extrox/93910.41 /CLONE=IMAGE:1635426 /UG=H4.7309 Homo supiens clone 2.3741 mRNA sequence	A4995925	1.67
	Myddwydd priferi Myddwydd ac y changledd y	A740515	1.67
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	To transmiss inches garden to the France support that the book of		1.67
		NM_003300	.67
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		A#205153	9.
	cyclin-dependent kinase inhibitor 1C (p57, Kp2)	WC2C3	2 3
	2n41d10.s1 /CLONE=INAGE:550003 /UC=Hs.90869 Homo sapiens clones 24622 and 24623 mRNA seq.	AA100250	8 3
	puratus) homolog 3 (actin-bundling protein, testiculur)	NM 020369	3
	(Po	NM_001975	39
		AF039196	99.1
	puramphary annual protein I	NM_022112	<u>3</u>
		NM_018162	99.
	a pigas	W2/2899	9 :
	amily, member 14 (herpesvius entry mediator)	KM_W2U5U3	8 9
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	852	NM_007167	39
		AF144240	99:
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	nember 28	M55580	9 :
		44209239	\$ 5
	tyrosine protein, T-STAR	NF069681	3
	Tipotate premi	NM_018992	39.
		(W592563	9.
		A-201291	8 3
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	rponent of Ra-reactive factor)	AV686235	3 9
	Caroun channel, vorlage-dependent, Litype, alpha 10 subunit	8E550599	99.1
	factor DATs	NM_004991	3.
	TO A TREE - 1 - 1 - CAN THE	AL050152	99.
		BF155672	9 :
	A sequence from clone 153614 on chromosome 6021.3-22.2. Contains the 3 and of the 2NE184 near for Knimsel Like vinc finance marketing	AM_018961	8 5
		NH 003408	8 3
	Compensus includes ap. A1344415 FEA=EST (A8_AREF=g; 4081621 (A8_AREF=est qp; 3b08.x1 / CLONE=INAGE; 1917879 /UG=Hs, 156082 ESTs A.I.	N344415	39
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aritales homedes (Orssophila)	NM_014807 1.66	
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har 2 interacting protein 8		
hypothetical protein FU12616		
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sindest-tree MATV interation site family member 3	NH_020435 1.66	
potassium immardy-rectifying channel, suptaintit   member 3		
period homolog 1 (Drosophila)	NW 002616 1.66	
90-18C005381.1 /DEF=Homo septions, come MGC.13287, mRM4, complete cas. /FEA=mRNA /PROD=Unknown (protein for MGC.13287) /DB ,XREF=qi:18623544 /FL=qb:BC006381.1		
nucleophosmin (nucleoler phosphoprotein 623, numarin)	AL353580 1.66	
2 9 87000 RD	NM_014080 1.66	
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glutanita dell'idrogenase 1	NM 005271	1.65
1	NM 003662	597
kinasin tarahy mambar 10	AB014606	59.
lectin, galactoside-binding, soluble, 4 (galectin 4)	NM_006149	1.65
hypothetical protein WE(10771	. NM_024506	1.65
reposit is	BF432550	1.65
secreted frizzed-related protein 4	NM_003014	1.65
special A1 arch sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	NM_002971	.65
emotifi A6	NM_001155	1.65
polassium innerally rectifying channel, substantly I, member 15	U73191	1.65
tumor protein 052-like 1	AF208012	1.65
tight junction protein 1 (zone accludens 1)	AA813018	1.65
Serine Paternase	NM_021947	1,65
neine granth factor, beta polypeptide	NM_002506	1.65
cphrin-L2	AW189015	1.65
retinitis pigmentosa 6 IP see regulator	NM_000328	1.65
Dry finger protein 358	NH_018083	1.65
wanye myakocytomutosia viral relatiad oncogene, neuroblastoma derived (avian)	AF320053	1.65
Institution receptor H I	NM_000861	9.1
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Corporator includes gb-JW024784.1 / DEF = Home supriens cDNV, FLU21131 fs, clone CASO6355. /FEA=mRNA /DB_JR8FF=gi:10437168 /M6=Hs, 28264 Home supriens mRNN, cDNx DK72p5641 M0024784	H AK024784	59.
DG7256411922 protein	AF245505	1.65
terbulka haplood expressed gene	NM_016585	1.65
cholinerys, receptor, nicotainis, beta polypepticle 4	NM_000750	1.65
protein Process procedurates, everpore type, N polypeptide 2	NH_002847	59 :
Together the control of the control	NM_014428	9
references and the second of t	NM_000358	6.
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hypothetical protein FLI11545	8F476502	3 5
deleted in coloractal carcinoma	NM 005215	59
capitard-binding protein-related protein 1	NH_018030	59:1
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hypothetical protein EU12619	BG252842	1.65
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ectodemal dysolesia   arbidratic	76037	3 5
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aldehyda dehydrogenasa 3 family, member A2	NM 000382	59
Type I protein phosphatase inhibition	NM_025210	1.65
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or gb.A.135548.1 /OEF=Homo sepiens mRNA (ONA DIGZP761G18121 (from clone DIGZP761G18121); complete cds. /FEA=mRNA /GEN=DIGZP761G18121 /PROD=hypx.	136548 1.60
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Jsher syndrome 2A (autosomal recessive, mild)	HM_007123	9.1
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consensus includes at: 8877397 /FEA=EST 708 XXEF = a; 10326173 //08 XXEF = cs; 60148543461 (XLONE=1846:3887936 //LE=14: 240140 Human DNA sequence from clone 153614 on BE877387	1614 or BE877397	91
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antyless-type MMTV integration site family, member 83	NH_003393	9.
catherin 10, type 2 (T2-catherin)	NM_006727	9.
Consonates includes gb:86391282 /FEA=EST //DB_XREF=gi:13284730 //DB_XREF=est:602417327F1 //LONE=IMAGE:4536582 //UG=Hs.306000 hypothetical protein FU10624	66391282	39.1
regulator of 6-protein signalling 6	AF 156932	29.
endacyte immunocyclodiin-like receptor, subtamity A (with TM domain), member 2	U82277	
death-essociated protein kinase 1	80003614	1.6
Consensus includes go:029310.1 /DEF = Human mRNA for unknown product, partial cds. /FEA=mRNA /PROD=unknown /DB_XREF=gi:704440 /U6=Hs.153445 Human mRNA for unknown pn D29810	own pn D29810	3.
ATPase, Class V, type 10X	AB011138	9.1
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I parawa ye do	NH_012403	- 60
hoseome building profein 1 homolog 180k0 (dog)	AA706065	3.
ymphocyte antigen 117	AF000426	9.
typobatical protein FU10770	NM_018211	3.
6DMF family receptor alpha 3	NM_001496	9.
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Corserva includes 95-3402242.1.1 / DEF = Homo supiers cDNA FU12359 fis, close HAMMA1002355, / FEA=mRNA / DB XREF = 0:10433814 / Jule = Hs. 296718 Homo supiers cDNA FU123591 AX0022421	2359 1 AK022421	3
Cuppel-type and finger (C2H2)	NN 005815	5

hypothetical protein FU10786	NH 018219	9
solute carrier tunity 16 (monocarbosylic acid transporters), member 7	AF049608	. 9
ATP-binding cassette, sub-family B (NOR/TAP), member 9		2 5
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hypothetical protein PR02176	NM_018515 1.59	
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hypothetical protein FUZ1369	NH 024802 1.59	
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Consensus Includes 90-M024851.1 /DEF = Homo sepiens cDNA: FU21198 fis, clone COL00220. /FEA=mRNA /DB_XREF=qi:10437259 /UG=Hs.306707 Homo sapiens cDNA: FU21198 fis. cl. AL074851		
aranda resistance protein ASS		
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Mdm2, transformed 313 cell double minute 2, p53 binding protein (mouse)		
hypothetical protein FU10300		
	NA_018051 1.59	

18.5	Consensus includes 0p. H31949 (DEF = Human la rearranged mu-chain V-region gene, subgroup VH-III, exon 1 and 2 /FEA=COS /DB ,XREF=cg1: BS254 /DG=Hs. 247923 Human la rearranged H31949	ed M31949	1.59
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NY	dymobypainogen 81	NH_001906	5
M1_01839	acyt-Coenzyma A dahydroganasa, C-2 to C-3 short chain	NM_000017	1.59
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GPI) mRNA, complete cds. FEA=CDS FEN=IgH PROD=immunoglobulin mu chain antibody MO30 /08_STEFE FE6453  HY_O14606  MAG08220  HY_O06233  HY_O06233  HY_O06233  HY_O06235	Lactabourin, alpha-	NM_002289	<u>.</u>
gH) mBNA, complete cds. FEA=CDS AER=IgH PROD=immunoglobulin mu chain antibody M030 /08_JRIEF NESAE3  MAG0820  MAG0820  MAG0820  MAG0823  H20 on chromosome 20q12-13.12 Contains the OCT gene for depachronne fuu/omerase (depachronne delta-isomer. AL13318  MAG02455  MAG0238  MAG0338  MAG0339  E1300256  MAG042712  MAG5864  MAG6695  E1300256  MAG02712  MAG5869  E13002712  MAG5869	IQAA0303 protein		53
NH_016466  AMODBED  NH_016466  AMODBED  NH_008213  NH_008213  NH_008213  NH_008213  RN_0081318  RN_008181  AD01946  NH_008181  AD01946  NH_008181  AD01946  NH_008181  AD01946  NH_008181  AD01946  NH_008181  AD01948  NH_014395  STEATS  AD01948  NH_008181	gb:W26463.1 /DEF=Homo sapiens immunoglobulin mu chain antibody M030 (IgM) mRNA, complete cds. /FEA=C05 /GEN=IgM /PR00=immunoglobulin mu chain antibody M030 /UB_JR		
AM00820  NU_006213  NU_006213  NU_006213  NU_006213  NU_006213  NU_006213  NU_006214  NU_006215  NU_006216  NU_006216  NU_006216  NU_006216  NU_006216  NU_006216  NU_006217  NU_006218  NU_006689  NU_006689  NU_006689  NU_006689  NU_006689  NU_006689  NU_006689  NU_0066899  NU_00668999  NU_006689999  NU_00668999	Nect domain and RLD 3	NM_014606	5
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B(002455) H20 on chromosome 13. Contains the DCT gene for semenogelin I and II and P13 (proteaus inhibitor 3, suin. ALO49767 MPL 202481 MPL 202141 MPL 202131 MPL 2021321 MPL 20213		NM_003613	2
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H20 on chromosome 20q [2-13, [2 Cantains genes for semenogelin   and    and    and    protesse inhibitor 3, stin, A.0.493767   Mv_022431   Mv_022343   Mv_022343   Mv_022343   Mv_022343   Mv_022343   Mv_02233333   Mv_0223333   Mv_022333   Mv_02233	Consensus scholdes gb./41.199318 /DEF=Human DNA sequence from clone RP11-124617 on chromosome 13. Contains the DCT gene for dopachrome tautomerase (dopachrome delta-ison	er AL139318	.5
NH, 022481 NH, 022481 NF, 022481 NF, 022481 NF, 020333 S76476 NH, 00338 NH, 003383 ND, 03383 NH, 003383 NH, 004, 38EF=9;2785901 /06=H3.167825 Homo supiens done 23607 mRM sequence Ar0381 81 One NT2RP2003533. FEA=mRM, 0B_XREF=9;7022701 /06=H3.140402 Homo supiens CDNA EL110580 fis AR001442 NH, 002099 E8300356 NH, 002099 E8300356 NH, 002099 E8300356 NH, 002099 E8300356 NH, 002099 E8300377 NH, 002097 E8300377 E8300	Consensus includes gb.4.049767 /DEF =Human DNA sequence from clone 172H20 on chromosome 20q12-13.12 Contains genes for semenogelin I and II and PI3 (protesse inhibitor 3, si		.59
## (2007) ## (2	hypothetical protein FU21065		<u>.</u>
NH_003733 S7676 A001131 A0001348 IO00348 IO00348 IO00348 IO00348 IO00348 IO00348 IO00348 IO00348 IO00348 IO1439 AND MARK / DE JREF = gi2795901 / V/G = Hs. 167825 Homo supiens done 23607 mRM sequence	hypothetical protein from done 24796	AF070596	.53
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ph:EXCO2778.1 /OFF=Home supiens, Similar to myosin light chain 2, precursor lymphocyte-specific, clone MGC:3479, mRIVL complete cds. /FEA=mRIVA /PROD=Similar to myosin light chain 2, precursor lymphocyte-specific, clone MGC:3479, mRIVL complete cds. /FEA=mRIVA /PROD=Similar to myosin light chain 2, precursor lymphocyte-specific, clone MGC:3479, mRIVL complete cds. /FEA=mRIVA /PROD=Similar to myosin light chain 2, precursor lymphocyte-specific.	/FEA=mRNA /PROD=Similar to myosin light chas BC002//8
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glutamate receptor, ignotropic, kainste S	SCT-SOC SEC
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POM (POM12) rat homolog) and ZP3 fusion	80000487
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hypothetical protein FLL23560	NN_024685
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dystrodrawin, beta	V672185
QW0874 protein	X80821
JANP response element-binding protein (RE-8Pa	NH_004904
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banor necrosis factor (Egand) superfamily, member 12	NM_003809	1.53
hypothetical protein MGC10818	NM_030568	1.53
UDP-4altbeta6kNk beta 1,3-galactosyltransterase, potypeptide 1	NM_020981	1.53
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varie 3	NM 018399	1.53
glucagon-lite peptide 1 mceptor	NH 002062	.53
Compensus includes 90:137198.1 / DEF = Homo septens (clone 8:381813) Huntingtons disease candidate region mRNA fragment. AEA=mRNA /DB XXEF=@:800519 /UG=Hs.233617 Homo: 137198	0:137198	1.53
transforming growth factor, alpha	AF149096	8
Consensus includes gb:NS4942 /FEA=EST /08_XREF=gi:1196262 /08_XREF=es1yw38b08.si /(LONE=IMAGE:244983 /NG=Hs.276590 ESTs	NS4942	5
horman bat (6	NM 004503	53
dead ringer (Drosophis)-like 2 (Bright and dead ringer)	NN 006465	1.53
hypothetical protein FU11827	NM 025093	1.53
serina/arginine repetitive matrix 2	AI655799	1.53
hypothetical protein FL11136	A1497781	5
small inducible optains AS (BAMTES)	NM 002985	3
uncharacterized bone marror protein BKO40	NM 018456	5
immunoglobulin superlarity, member 4	AF132811	5
mentrane-spanning 4-domains, subtamity & member 5	NM 023945	5
dictatopt homolog 1 (Xenopus Izeris)	NM 012242	1.53
productin	NM 000948	53
Sjagnen syndrome entigen A2 (60KD, nibonucleopratein autoantigen SS-A/Ro)	AK024044	1.53
hypothetical protein FLI20378	NM 017795	1.53
DEAD/M (Asp-Glu-Ma-Asp/Mis) bas podypeptide. T chromosome	AF000985	1.53
floroblast growth (actor 16	NM_003868	1.53
oran-liperity appopulate inhibitor in	NH_001704	1.53
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branchbional activator of the c-tos promoter	NW OCCOC	3 9
hypothetical protein FU20255	NH 017728	3 2
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) FEA=EST 708_XREF=gi:1126334 708_XREF=estrys50h10.s1 / CLONE=IMAGE:265219 /JJG=Hs.26968 Homo sapiens mRNA from chromosome Sq21.22.	clos N21364	2
votein, Y-linked	NM_003308	5.5
nddodrudii 2	NM_005013	1.53
Proportional protein FU   1265	HM_024877	1.53
HIOT prices	NF225421	1.53
podstanni invanthy rectifying channel, subhamiy I, member 12	MM_021012	1.53
CLIA-MOI transcription complete, subunit 4	U71268	1.53
C-type (catcum dependent, carbonydrate-recognition domain) lectin, superfamily member 12	AF313468	1.53
mannosyi (apra- i.5-)-gytoprotem beta- i.4-Ki-kerygucosamnyiitansiense, isoensyme A	NM_012214	1.53

NH_00550 phospharylase bisnes, apla 1 (muscle) wrs.3 hormolog B (f. despans) wrs.3 hormolog B (f. despans) wrs.3 hormolog B (f. despans) consensus includes giv.M.1901193.   DEF = Hormo sapiens mRNV; cDNA DIVZp5478026 (from clone DNZp6478026). /FEA=mBNA /DB_138EF=gi:336883 /UC=H1, 283862 Hormo sapiens mrd M.200139 ECO06333 wrs. despansion includes giv.M.190190   14 ECO06333 wrs. despansion includes giv.M.191281 fis, clone DNA EU13283 fis, clone CNARC1001113, highly similar to Hormo sapiens cDNA FU14151 fis, clone HAMM MU148255 Consensus includes giv.M.023345, 1 DEF = HOMM FU13283 fis, clone CNARC1001113, highly similar to Hormo sapiens cDNA FU14151 fis, clone CNARC1001113, highly similar to Hormo sapiens cDNA FU14151 fis, clone CNARC1001113, highly similar to Hormo sapiens cDNA FU14151 fis, clone CNARC1001113, highly similar to Hormo sapiens cDNA FU14151 fis, clone CNARC1001113, highly similar to Hormo sapiens diaphanous 1 (HDIAI) mRNA. /FEA=mRNA /DB_1XEF=gillar RNA /DB_1X	NM_004739
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eceptor delta locus	NM 003382
	X06557
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cytochrome P450, subtamily IIC (mephenytoin 4-hydroxylase), polypeptide 18	NH_000772
integrin, beta S	AL048423
IGMAN50 gene product	NM_014638
hypothetical protein FU22059	
Consorns includes gb.XIQQ2363.1 / DEF = Homo sapiens cDNA FU12301 fs, clone MAMMA1001858. /FEA=mRNA /DB_XREF=gi:10433745 /UE=Hs.287511 Homo sapiens cDNA FU12301	-
ando-oncopane tyrosine tousse	NM_006343
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dystrobrawin, alpha	046745
hypothetical protein DVZ1p76100113	NM_018409
solute carier tamity 21 (prostaglandin transporter), member 2	NM_005630
striated muscle contraction regulatory protein	H96843
nedesporin 85/0	Y08613
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hypothetical protein FU11264	NM_018371
ets variant gene 3	116464
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CRRF35 leukocyte immunoglobulin -lilu receptor	NM_00678
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arin related protein 8	AL050178

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IGAN 614 protein		
vanilioid receptor subtype 1		
hypothetical protein FU12673		
RDMD670 protein/acinus	NH_014977 . 1.52	
adaptor-related protein complex 1, mu 2 subunit		
transcriptional adaptor 3 (ADA3, yeast homolog)-title (PLOK histone acetylase complex)	AL117487 1.52	
biller cell lectin like receptor subfamily C, member 4		
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degenerabies spermutocyte homolog, fipid desaturnae (Drasophilia)	_	
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hypothetical protein FU11292	2	
activity, alpha 1	M95178 1.52	
DVSZ-related protein		
disphanous homolog 2 (Drosophila)	NM_007309 1.52	
CDC14 cell division cycle 14 homolog B (S. cerevisiae)	AF064105 1.52	
Ral guanine nucleotide exchange factor Ral6PS1A		
biller cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	NM_002255 1.52	
soldta carier family 4, sodum bicarbonate cotrasporter, member 4		
nuclear membro subhamily 2, group C, member 1	M21985 1.52	
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	observations ( but a	NA_000033	<u> </u>
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	programmed death liqued 2	NM 025239	151
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	RNA binding motif protein 9	AW149379	1.51
	organic control transporter-like 3	NH_004256	15.1
	reported potent	NM_016387	5.
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	hypotherical protein FU13197	NM_024614	1.51
	coagulation lactor il (thrombin) receptor-like i	BE965369	1.51
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	solver call immunospoodini-lake receptor, two domains, short cytoplasmit (asl, 3	NH_012313	1.51
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### 177110  1004 sequence from closer #FF111 (1512.2 on chromosome \$421.3.2.2.2 Centulan the gares for mydinologopedendery() ejycoprotein VGC, (pa.4.2592.2)  28.20.1  28.20.1  28.20.1  28.20.1  28.20.1  29.20.20.20.20.20.20.20.20.20.20.20.20.20.	mention house coherentials (1 emonth muscle	NM 022844	1.5
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Common part of the control of the co	Compensus includes do AL031686 /DEF = Human DNA sequence from clone 981L23 on chromosome 20q12.1-13.2. Contains a Krueppel type 2	-finger protein pseudogene, a ZNF127 pseux AL031686	1.5
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Comments includes @ MO2453.1 / OEF Home states ONA F120900 fs. close ADM03593. FEA.=mBNA ///B 2005661 / MC=Hs. 306687 Home states CONA F120900 fs	AK024553	9
SP110 nuclear body protein	NM 004510	8
dasu NK-restriched T dell associated molecule	NN 019604	8
done FLJ 1727	NM_016414	3:
protein A	NM_019858	8.
COTSON THE CONSONAIS FEAREST NO. TREF = 93:3769734 NO. TREF = est:2083403.11 /CLONE=INAGE:1953029 /UG=14:306019 ESTS, Weally similar to ALU7_HUMAN ALU SUBF?	F# A207792	3.
similar to 568401 (cattle) glucose induced gene	NM_012261	3.
hypothetical protein M625457	8000038	3.
Neutrine rich ropast (in FUI) interacting protein 1	BF965566	3.
hypothetical zinc finger protein FU14011	NM_022103	3.5
Opstanla muscularum of mause, human homalog of	AL049215	2
PAO1346 protein	NM 031269	95
greeth hormone 1	NM_022561	35
ring finger protein 17	NM_031277	8:
solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	A827990	05.1
secretary carrier membrane protein 1	AL049223	8:
Verrocheldtase (protoporphyria)	NM 000140	3
haptoglobin-related protein	NM 020995	8
Consensus Includes gb-XX024455.1 (DEF = Homo supiers mRN4 for FU0004? protein, purtial cds. (FEA=mRN4 /REN=FU00047 /PR0D=FU00047 protein /DB_XREF=ei:10440423 /UG=Hs.		8.
caldum channel, voltage-dependent, alpha 2/delta subunit 2	NM_006030	1.50
Corsersus includes gb-XX026682.1 /DEF=Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306866 Homo supiens cDNX: FLU23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306866 Homo supiens cDNX: FLU23029 fis, clone LNG01883 /UG=Hs.30686 /U	d AX026682	3.5
c-enyt binding protein	NM_012333	8.
POAMOR28 protein	AK025372	8.
chandratin suffite protecypycan BEHJA/brevican	A/205180	05.1
dynain, cytoplasma, intermediate polypeptide 2	AF250307	3.
similar to NYOSIN HENYY CHAIN, CARDAK MUSCLE ALPHA ISOFORM (MYHC-ALPHA) (M. musculus)	AK000947	8.
phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	NM_005027	3.
Consensus includes gb-J4478300 FEA=EST /08_TREF = gi:4371526 /08_ZREF = est:471526 /08_ZREF = est:471526 /0.1 / TLONE=IHAGE:2160504 /UG=Hs:192789 ESTs, Wealby similar to ALUG_HUMAN ALU SUBSF A478300	1 AI478300	3.5
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hypothetical protein MGL2376	NM_023930	8.
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phospholipid scrumblase 1	NM 021105	1.49
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homolog of years ATP 12	AF070584	1.49
NACH dehydrogenase (ubiquinone) 1 bets subcomplex, 8 (1940, ASH))	AA723057	69:1
Imphocyte artigen 95 (activating MK-receptor, NK-p44)	NM_004828	1.49
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k sampe (kuky) akuta bateu (katea) 3	NM_005751	£.49

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upstrem binding transcription factor, RNA polymerase I	X56687	67
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Consensus includes go 24 234235. I DEF = Homo saptens clone KM 36 immunoglobulin light chain variable region mRNA, partial cds. IFA=mRNA IPROD=immunoglobulin light chain variable		1.49
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property of detection of the control	NH_014709	1.49
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protein hyrosine phosphalase, receptor type, 6	NM_002841	1.49
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went commentations document (II), and cytoplasmic domain, (semaphorin) 6A		1.49
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call receptor alpha locus	AECOOP 3
Consensus includes gb:8E794663 / EA=EST /DB_XREF=gi:10213861 /DB_XREF=gi:001590458F1 / CLONE=IMAGE:3944483 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 744653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 744653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 744653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Homo storens (DNA PU 14089 Hs. Clone PM BE 746653 / UG=H3.305668 Hs. Clone PM BE 746653 / UG=H3.30568 Hs. Clon	A FU14089 hs, clone MA BE/94663
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profine-rich protein BstM subfamily 3	NH_006249
putable 6R6 protein	NR_00/354
salctionin gene-related peptide-receptor component protein	NA_014478
IQAA1157 protein	AB032983
hypothetical protein FU20489	AW149696
symbophin, beta 2 (dystrophin-associated protein A1, S940, basic component 2)	M762021
maufin-like growth factor binding protein 4	NM_001552
dekt effecter protein 2	8005406
Proceduration or other FU22222	NM_024648
ANS anothers Sale (S. convision)	NM_004849
mutit entatocroteinas (2 (merrophase elastase)	NM_002426
ATP-binding cassette, sub-family 6 (WHITE), member 1	U34919
LIM domain binding 3	AA211481
pyrdecan I	NM_002997
transducer of ERBS2, 2	064109
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00F2P5641122 protein	221900152
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hypothetical protein DKZLp434P144	AL136868
<b>Consensus includes gb:AA837026 /FEA=E77 /08_XREF</b> =gi:2912225 /08_XREF=est:0909c12.s1 /CLONE=IMAE:1439350 /U6=Hs. 163549 E51s	970/57
Fe theganest of legs, high efficity is, receptor for (CD64)	X14355
Phononel protein S6 kinasa, 90KD, polypeptide 5	AF074393
poly (ADP-ribone) glycothydrolene	NM_003631
cyfidin, benie protein of sperm head cytraskeleton 2	NM_001340
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	hypothelial protein DG72434M1923	KM_0309/4	2 :
	major Nistocompatibility complex, class II, DP alpha I	A128225	2 2
	understype RIM integration is transp. member b  Miderate Research RIM integration is transper b  Miderate River and Miderate Ri	.88. AF339787	.36
	Comments included by Manager (AMA) and Manager (	7_H AWS03390	1.36
	BQ2-flee 11 (apoption) buildings)	NM_006538	1.36
	interfection 1 receptor, type II	KM_004633	.36
	denomodomain halicase DNA binding protein 2	NM_001271	e :
	definency membra, incolarie, delta polypeptode	NN 006850	2 2
	FIGURALIA 4	AW450751	1.36
	of a children in the control of the	NM_014256	1.36
	neght related gene		1.36
	Commercia ph. J. 203728. 1 (DE From supiers tone morphogenetic protein BMP (BMP) mRNA, partial cds. /FEL=mRNA /EEN=BMP /PROE-bone morphogenetic protein BMP.	MP' AF203728	1.36
	collagent type XI, sights 1	NM 000816	3.5
	gamma-ammonday/ n recipios, gamma c 	AF169148	1.36
	arbeits of the control of the contro	BF001670	1.36
	Cardon Alched Heins serroms viral (v-tyr) ancogene hamalog	80002836	1.36
ć	NADH dahydrogenase (ubiquinone) 1 beta subcomplex, 7 (1800, 818)	M333/4	<u> </u>
5	and the curve first and thresporter), member 3	NH 000120	<u> </u>
4	spannes sprawer in motioner in the motion of	AI659561	1.36
4	•		

LDS1-behandzing prothein MUDE1, rat homolog	NM_017668	1.36
methyl Cp6 bhrding protein 2 (Rett syndrome)	KM_004992	1.36
IDAGES gane product	AF201292	1.36
gannas aminobulynte acid (GABA) A receptor, alpha 4	902000_MN	1.36
PRO255 protein	NM_014124	1.36
Carbonic serinychase XV	NM_012113	1.36
cereballs i procusor	NH_004352	1.36
interfacion 15	NM_000585	1.36
Communicate Included go. AVIO2 4479.1 / DEF = Homos supiens cDNA: FLU2 1226 fis, close COL00721. FEA=mRNA /DB_XREF=gi:10437291 /UG=Hs. 306715 Homo supiens cDNA: FLU2 1226 fis, cl AKD24879	:U21226 fis, ct AX024879	1.36
byptone defta 1 · ·	KM_012217	1.36
TU1281-TY protein	NH_016575	1.36
Conserved includes gb-ALGBG215.1 / DEF = Homo supiens mRNA: cDNA DVF2658610323 (from clone DVF2658610323). FEA=mRNA / DB_XREF = gi-5262706 / UG=Hs. 102301 Homo supiens n ALGBG215	forno sapiens n AL080215	1.36
erydd farnardyddon fator I dia	AL133024	1.36
Leaf QL/Ayriphoma, 11A (bric finger protein)	NM_022893	1.36
Shiptomy opplanese (serotone) receptor 18	M81590	1.36
Cariobacomi protein 2	8C001433	1.36
interface in receptor, type	NM_000877	1.36
gover arrementation ratio ?	NM_005260	1.36
CONTRIBUTION IZ Open reading frame	NM_001585	1.36
Manual of the state of the stat	NM_004742	1.36
The state of the s	NM_014786	-36
putable Reconstructions (Lampio 2	NH_016347	1.36
INTEGER - ACTIVITIES FALSE 4	AA810268	1.36
ethylation repeat, all a homolog	NM_006020	1.36
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a distribuyin and metalloprotecture domain 30	NM_021794	1.36
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hypothetical protein MKSS28	111372	1.36
retmatching broken	NH_000326	1.36
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dust-spacificity tyrosine- (1) -phosphoryston regulated kinase IA	052373	1.36
aldo-bate reductase family 1, member 01 (deta 4.3-ketosteroid-5-beta-reductase)	NM_005989	1.36
E-tector, properties	AF349679	1,36
Moth-frachom syndrome candidate 1-like 1	NH_023034	1.36
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endin 4		1.36
NAO lihase	BE551347	1.36
randeer entigen Sp100	NM_003113	1.36
ghooprotein 2 (symogen granule membrane)	NM_001502	1.36
IZMA732 protein	AF155097	1.36
calmodulin 3 (phosphorylase binase, delta)	NM_005184	1.36
AD*-thoughtunisterabe (NAD*; poly (AD*-those) polymerase)-like 1	NM_006437	1.36
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	grathen byreades phosphalase, receptor type. H portpettode 2	NM_000074	1.36
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	reported to control of the control o	139212	1.36
	calculation of contract of the	NM_007058	1.3 %
	DMA (cotmises S.) amethyltrastions 3 alpha	NM_022552	1.36
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	Importation protein FU204S	AL136872	9. 7.
	Companius Inches CANO27217.1 (DEF = Homo sapiens (DNA: FLL23564 fis, clone LNG10773. / FEA=mRNA /DB_XREF=gi:10440296 /UG=H3.306913 Homo sapiens (DNA: FLL23564 fis, cl AXO22277	AK027217	9
	genne globanytransferne-Ste activity 1	NA_004121	9
	hypothetical protein RJ10970	NM_018286	9.
	protein lakes C, appla binding protein	NM_012407	9.
	6 protein-coupled receptor khase-interactor 2	NM_014776	9.
	hetsevine H-methytzusstersse	N40285	e :
	transducin-Ca enhancer of soft 1 (E(ss1) homelog, Orasophila)	NW_005077	9. :
	SRY (see determining region 1) -box 30	NM 007017	3.7
	shoutshale cycloth/transferse 1, choline, siphs lootom	/10500 WN	9 7
	cytachrome P450, subfamily IXA (cholestard) side chain cleavage)	NM_000781	9 3
	erythrocys membrane protein band 4.9 (dematin)	NM_001978	9.
	endocoleth-like 4	NM_016109	9.3
	ecicle receive, mu	695710	9 :
	Consenses Includes ab AL136967 (DEF = Human DNA sequence from clone RP1-149M 18 on chromosome 6 Contains ESTs, STSs, 655s and (p6 islands. Contains the natural killer cell p44 ret AL13696)	4 AL13696/	9. 5
	DAS2, member DAS oncogene family	AX024417	9
	hypothetical protein FU14360	N38/51	9
	Concensus includes go.NV741657 /FEA=EST /OB_XREF=gi:10859238 /OB_XREF=est:NV741657 /CLONE=CBMA.GO1 /UG=Hs.154085 leucine zipper protein l	AV/4165/	9
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	DRTZ8600919 protein	4001660	2
	Consenses includes objUC021569.1 (DEF=Home sepiens cDNA FL11507 fs, clone HEMBA1002166, (FEA=mRIA /DB_URE=9110432775 /ULG=93.11434 Home sepiens cDNA FL11507 in Anna taxon to a sepiens contact to a s	# AND 1303	2 2
	KDAA0790 protein	1000130	2 4
	DNTP444C153 protein	1119601	2 2
	runt-related transcription factor 1 (acute my-dood leutemia 1; am 1 oncogene)	NM 006517	95
	south carier tarity 16 (monocarbosytic acid transporters), member 2 (putative transporter)	NM 002053	2 2
	natural killer cell receptor, immunoglobulin supertamity member	RF673888	2
	spadde-type PO2 protein	NA 005549	1.36
	potassium voltage-gated Channel, shaker-et-lated subhamity, member 10	NM 004791	1.36
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	Consumes behave aby A0216901 (AEE Home supiers DNA FULL 1628 fts, close HEMBA 1004238, FELS=IRMA (AB XREF=gi:10432926 / IGE=Hs.306610 Home supiers CDNA FULL 1628 ft A021690	h AK021690	1.36
	translutarinase 2 (F potypeptide, protein-glutarrine-gamma-glutarritarrase)	M98478	9.
	med. homolog 3 (E. coli)	ABU3968/	9 2
	calcins dramet, voltage-dependent, beta 3 subunit	Y09908	2 %
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	mmens of programmy programmy operatory with the state of	BE223030	1.36
	south these AMP described residency from July 1975.	8F246917	.36
	22 transcription factor 3	A640363	<u>.</u>
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	hymphosyte antigon is complex, locus 0	136861	9
	guenyide cyclese ectivator IA (retinu)	NN 014519	1.36
	Little froger protein 2.2.	NM_017705	1.36
	hypotheria transmission in the second	M34715	1.36
	Hartween pour con	86223341	1.36
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	To contempt the set of	NM 003577	
	homeless of secuse quadries (OI) domain RIV, bringing profession	AL031781	1,35
	ATT-Back, H+ transporting, hyposomal (notuclar proton pump) 42:0	AW024925	1,35
	hypotherical protein DIT 2656/091	NH_030915	1.35
	IGM111 protein	AF091081	1.35
	Improgramia (improgramia fantus 4)	NM_002479	£
	Consumes includes go.A.[O49646, ABE = Human DNA sequence from clone RP 4-568F9 on chromosome 20 (contains the ZNF 133 (sinc finger protein 133 (clone pHZ-13)) gene, part of a gen ALD49646.	gen AL049646	1.35
	homotog of Amopus Custom	MM_022111	2 :
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	hypothetical protein EU10199	NM_018022	1.35
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	decident comment receiver italiay, member i	SIFIL	9
	hapatoryta nuclear factor 3, beta	AI693985	£.
		NM_005149	56.
	Tarney web sequence stentienty &, member A l	MM_016255	3
	transcription factor 7 (T-cell specific, HMG-box)	AW027359	1.35
	Pynerate dethydrogenuse complex, lipoyl-containing component X. E3-binding protein	NM_003477	1.35
	collagen, type N, alpha 1	Al922605	1.35
	anthyrin report domain 3	WM_020639	1.35
	catherin 3, type 1, P-catherin (placental)	NH_001793	1,35
	budyngshills, subtamily 1, membar A1	NM_001732	1.35
	matrix metalloproteinese-Res 1	NM_004142	1.35
	CUG tejaki repad, RMA bindng protein 2	NM_006561	1.35
	Enting sercome breakpoint region 1	AL031186	1.35
	Consensus includes gb:U5835.8.1 /DEF = Homo supiers done R.2 Ech8-3 R.2 (<-ch8-3) mRNA, purisi cds. /FEA=mRNA, /GEN=<-ch8-3 /PR00=Erh8-3 R.2 /D8, 2REF=gi:3323390 /UG=Hs.3( U88358	.3( U88358	1.35
	cytodycome P450, subfamily IIE (ethanol-inducible)	102843	1,35
	historine H4 receptor	AF312230	1.35
	Randslast growth factor 7 (heratinocyte growth factor)	NM_002009	1,35
	paired bas gene 5 (B-cell lineage specifik activator protein)	NM_016734	1.35
	phosphomotoynwete carbonytinase 2 (mitochondrial)	NM_004563	1,35
	Consumbus includes gb.AM979018 /FEA=EST /08_XREF=gi:8170301 /08_XREF=est:EST391128 /UG=Hs,132670 ESTs	AW979018	1.35
	cytochrone P450, suchanity NF, potypreptide 8	AF133298	1.35
	phosphodesterse 40 Interacting protein (inyonnegalin)	A1821791	1.35
	sperm protein associated with the nucleus, A chromosome, family member A1	NM_013453	1.35
	unneth A2 pseudogone 3	M62895	1.35
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	COMPANIES BECAUSE DESCRIPTORS THE SECOND SEC	H94842	3 5
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i	serbo (or cysteins) proteinsse inhibitor, clade 8 (coaffurnin), member 13	A001696	1,35
	The machine A	NM_019105	1.35
	Consumus includes go.AZ7413 (DE =Horno septent partial (SVH3 DP29 gene for immunoglobulin heavy chain V region, case 1, cell the VII 116 /FEA=(DS /08_XREF=gi3573089 /UG=H5		1.35
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	March alpha March alpha	NM 005422	1.35
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	gup junction protein, beta 3, 3100 (comeanin 31)	AL121988	1.35
	mysten engodendrocyte glycoprotein	018800	1.35
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	ATP symbase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardae muscle	AU140931	1.35
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DOUGH (Appended to property of polyperty)	NA_004/28	
COCOMING OPPICAL AND THE COLOR OF THE COLOR	A-061194	5 3
HARATE REPORT OF THE TOTAL TOT		
received a transplantation of the content of the co	NN 003476	2
GAOOTS arterin	NH 025010	Ž
zbr. (Ingar protein 22 (10.01 16)	ALS67808	7
kulliterin B, plasma (Petcher factor) 1	NM_000892	1.34
hypothetical protein DIV71p434E2220	NM_017612	Ž.
manther of NYST tarmly histone except transferases, homolog of Orosophila MOF	AL050395	<u></u>
hypodedical protein FU12193	NH_024984	7.
India system-essociated membrane protein	NM_002338	Ž
Epitalisa megitar 19	NH_006143	<u>.</u>
(MACSE) protein	MM_014907	<u>.</u>
Authorized BOAR (1/02). 1 (1/02) = From Suprems (100% 24+0) min'nt Sequence. 1/10. = India 2.   1/10. = 1/10. = India 2.   1/10	NW ODIESE	
Proposition of the Control of the Co	NH 019062	3
systems muscode brinding protein (6 protein), alpha inhibiting activity potypeptide 1	AL049933	7
dinc Ringer protein 106	NM_022473	<u></u>
Conserve Includes gb:\M884814 \FEA=ES1 \DB_XREF=gi:S589978 \DB_XREF=et:\M85405.x1 \T\ONE=IHAGE:2431664 \DG=H1.21964 ES1s	A884814	<u>.</u>
mysain, light polypaptides 5, regulatory	NM_002477	<u>.</u>
Conserves includes got 18056029 FEL-EST /OB_XREF=e1:10809925 /OB_XREF=e1:7X07103.x1 /CLONE=114AEE:3443836 /UC=Hs.174910 ESTs. Weakly similar to dysterlin Haspiens	8F056029	<u> </u>
hypometral protein [L2055]	NM_017875	<u>.</u>
Programmy Section 2	AA8830/4 AE031136	
structure and st	8003126	1
Consumus includes gb.XII 15806 ff Eb. EST (08, XREF = gi:11007327, (08, XREF = est-XVII 45806 (XLONE=NEMBA1005894 / INE=Nt. 296664 Home sapiens (DNA FLI11776 fs., clone HEMBA AVII 45806	1 AU145806	~
Consumus bricholos giv/F 107846 (DEF = Homo supiens neuroandocrine-specific Golgi protein p55 (XLalphus) gens, ezon XL2 and complete cds FEA=mRNA (D8_XREF = gir4206779 /UG=Hs AF 107846	s AF107846	1.34
hypothetical protein PR02949	NH_018544	<u> </u>
MARKOTOTA PITURE INTER-	A54213	5
event with produced to the PSE (0) 446 from close PLME (1006979	NM 020377	7 2
Frograph homeobox protein 4	NM_016358	ž
aquaparin 2 (collecting duct)	NH_000486	Ž.
Fabor enty protein 21		Ž.
Consenses includes gs-AL11747.1 (DEF = Home supiers mRNN; CDNN DEF 2586-MG I7 (from done DEF 2586-MG I7), FEB.= mRNN, DB, 2REF = gi-5511855 (VIG=Hs. 3063-42 Home supiers	AL117447	ž.
CONSTRUCT (1907) AND ADMICED OR 1 (1907) AND ADMICED O	AK022063	<u> </u>
shows a second double for the construction of	AV645756	Ž
sinches (marchine sinches)	NH 006656	7
guarative nucleocide binding protein (6 protein), beta polypectide 3	NM_002075	7
Fart problem	N732960	7
Consumus includes gb-MB24954 /FEA=EST / DB_MEF=gi:5445625 / DB_MEF=est=nb0407.x1 /CLONE=INAGE2.2304684 / UG=Hs. 157429 SRY (sex determining region Y)-box 3 /FL=gb:NI M824954	N824954	 7.
CAAVOX proteins	66530481	<u>.</u>
Amenda Del (1)	MM_01/410 AF249114	5 2
Nemopotoni, beta	A 343114	5

untendo)	200000	:
production of the first of 2 PM LEGIS ACC subdomits managed 23	CE 120 MM	5 :
MM_QUISO  Francis principles of principles of the principles of th	MM_W01932	<b>.</b>
CONTRACTOR OF THE PROPERTY OF	1 1 AXO22363	¥.
A CONTRACTOR OF THE PARTY OF TH	NM_024690	<del>.</del> .
CATHER, ESP LAS SEVERI-PASS 6-1779 PECEPIOR 2 (Namingo homolog, Drosophila)	087469	7
Coll recipion garman locus	AC006033	1.34
AF Sapi 4 protein	NM_020380	<u>.3</u>
T call receptor gamma constant 2	H13231	1.34
Indiangements nuclear ribonucleoprotein U (scaffold attachment factor A)	013413	1.34
papidytordy isomerase E (cyclophiin E)	BF511556	1.34
hypothetical protein FLZ0509	NM 017851	7.
hypothetical protein FU10339	NH 018063	
TGFB-induced factor 2 (TALE family homeobou)	N 021809	
much 24 Intestinal	AE007194	
chromome 21 open medina trame 68	NA 024044	5
adaptor-related cortices carried automore	1111_VC+3+4	
Preside IA	4500061	5
strong of the factor for the sub-office and strong files	Arunayai	1
CONSTRUCTION OF A STATE OF A STAT	MM_001505	5
W. S.	M/1610/	<u>.</u>
Formula property of the Person Land Control of the Person Line of the	61-590317	¥. :
months instructionary with a party is minuted to contain protein to	KM_002114	<u>*</u>
Improving money is the state of	KM_000457	<u> </u>
CONTRACTOR STATES INTERFERENCE EXPOND EXPONDE THE TOTAL UNIT TOTAL UNIT TOTAL DISTRIBUTIONS THE STATE STATES TO THE TOTAL STATES THE TOTAL DISTRIBUTION OF THE STATES THE TOTAL DISTRIBUTION OF THE TOTA	1) ALO49233	1.34
INTERNATIONAL STATE OF THE PROPERTY OF THE PRO	24848	Ť
7. TO THE PARTY OF	NH_001452	-34
and a severes nominog 1 (Arcocphila)	AA700167	<u>.</u>
	M57765	7.
UN domain linese 1	NM_002314	7.7
Emiscryddon factor 3 (E.2A immunoglobulin enhancer binding factors E12/E47)	A871234	7.
hypothetical protein FU20244	AL390133	1.34
brandription elengation factor 8 (Skil), polypeptide 1-like	BE964043	1.34
the finger protein	A349848	1,34
ganadotopin-regulated testicular RNA helicase	NM_013264	7.
hypothetical protein FU2328.2	NM_024816	1,34
signal transducer and activator of transcription 1, 91kD	BC002704	1.34
heretity hair, exists, 8	NM_006771	1.34
Conservation includes giv.M. 15665 FEA=EST 08_ARF = gi.1728480 F08_ARF = est: #20008.si /CLOHE=IMAGE: 50.2503 /UG=H1. 27370 Homo sepiens many, cDNA DICI256400122 (from	AA156865	<u>~</u>
hypothetical protein FU10634	NH_018163	1.34
CONSTRUCT OF ANOLY 1895. I DEF = Home supiens CDNA FUL 1833 Fs, done THYRO1000676. FF BA= mRNA DB_REF=9:10435969 /UG=Hs, 296745 Home supiens CDNA FUL 1833 F. AR023895	: AX023895	ž
Consuments includes gd:A439416 /FEA=EST /08_ZREF=gi:4304169 /08_ZREF=estig04504.11 /CLONE=IMAGE:2140495 /JJG=H1, 165728 E5T3	A439416	<u>*</u>
calchen channel, vortage-dependent, alpha 16 subunit	AB012043	Ē
transcription factor AP-2, again, (activiting enhancer brinding protein 2 alpha)	BF343007	1.34
i protein-caupad receptor, family 1, group 5, member 8	NM_016235	1.34
	D87433	<u>*</u>
LOCATION OF THE STATE OF THE ST	Y10259	<u>.</u>
Transfer of the state of the st	NM_018496	<b>X</b>
ode SW results menter 2	NM_UU3833	1
hypothetical protein PP1663	AI 041124	
Cooks, lappa	NM 005212	5 2
actition A reception, type IB	NM 020328	5 2
mutabled in coloractal cancers	NH 002387	2
hypothetical protein FU11715	NM 024564	
sonie hedyshog (Orosophila)	NN 000193	5
Consenses includes gb-M057637 /FEA=EST /08_XREF=gi:3331503 /08_XREF=ext:0931h06_x1 /CLONE=IMAGE:1667483 /UG=Hs. 234898 ESTs, Weakly similar to 2109260A 8 cell growth 1 A1057637	A057637	7
CE-148 protein	NM_016078	<u>~</u>
Consuments includes gb.AW973235 FEA=EST /DB_XREF=g:1163081 /DB_XREF=est:EST385333 /UG=Hs.293697 ESTs	AW973235	.34
T. Carrier	NM_006853	1.34
homogentisute (1,2-dicargentisute (homogentisute ozidase)	A478172	<u></u>
matrix Ca protein	006000 WN	<u>.</u> .
Contentions includes gordB0773.1 /DEE Filamen EST done 42944 marrier transposon Hamari sequence. /FEA=mRNA (DB_XREF=gi:2231376 /UG=Hs.121580 Human EST clone 42944 marri US0773	U80773	<u>.,</u>
CONTROL OF THE STATE OF THE STA	AK025363	<u></u>
putabre honrecoonlan transcription Tactor 1	AA927671	<u>~</u>

Mab I, myaloid ecotropic viral integration site 1 homolog (mouse)	NR_002398	
pre-TAM call associated protein	KM_D04908	5
complement component 1, q subcomponent, receptor 1	#1,508Z	•
exharyotic translation factor 3, subunit 1 (alpha, 35kD)	MM_003758	<u>.</u>
phosphalippes A2 receptor 1, 18040	NM_007366	<b>X</b>
graph erret-coult.?	80006454	Ž.
proposin I, shektul, fast	NM_003282	<u>~</u>
NOANS 34 orders	AW151108	<u>*</u>
harman number and the second of	N21184	7.3
Incorporate action [1] 156	NM_024682	2
Bark articles of musa zirk finer homodomain 4	NM_024721	Ţ.
directionming branched chain preserving (2 component of branched chain keto acid dehydrocenase complex; maple syrup unine disease)	M19301	1.34
RAGE member NS ercoron farily	BC003617	<u>.</u>
referent brank Little	NM_015719	ž
and the state of t	KM_030631	2
	KM 006059	<u>-</u>
A BATTAL A STATE OF THE STATE O	AV716798	Ť
O O O O O O O O O O O O O O O O O O O	010537	35
ingular process zero (Charcoc-Hane) coch neuropathy (B)	WH 000290	3
phosphopycrate mutase Z (muscle)	NY OFFICE	
hypothetical protein FU10921	7/3610 NA	
hypothetical protein	0700TO	1
(GL35 protein	NA_015962	<u>.</u>
collages, type XIII, siphs 1	502500 WA	•
IQAN DBS protein	AUTOUS/6	1
inoutin-title growth factor binding protein 5	AR15/548	5
B-call CLAyriphons 10	AF082283	<u>.</u>
Consumbles gh./4652176.1 /DEF=Homo sepiens done 24457 mRNA sequence. /FEA=mRNA /DB_XIEF=gi:3360487 /UG=Hs. 158529 Homo sepiens clone 24457 mRNA sequence	AF052176	<u>.</u>
IQAA0551 protein	R59093	÷.
Conserses includes gb304178.1 / DEF = Human abnormal beta-he:osa-minidase alpha chain (HEXA) mRNA partial cds. /FEA=mRNA /DB_XREF=gi:184001 /UG=Hs. 166299 Human abnormal 104178	104178	7.
H-acetylghorsamine-phosphate mutase	AV727934	-
MAD, mothers against decupentaplagis hornolog 4 (Drosophila)	U44378	<u>.</u>
desnocolin 2	NH_U04349	
net estated brancopolon factor 1 (acute myeloid feukema 1; and 1 oncogene)	M-001/34	
cold automitian syndrome I	WH 000739	2
Openheidy Negroo, muscanny C	AK001827	7
Mathematics and a second secon	AW008921	7
CONTROL GOARDON GOARDON TO THE TAIL TO THE TAIL	NM 003279	7
Organia (1947)	NM 004842	7.
A Lander (V Any Daniel )	NM_017949	<u></u>
Information programme (Section 2)	K0320S	<u>.</u>
promoterial prima acts controlled (16.02 activation component of Ba-reactive factor)	NM_001879	7.
THE Annual and an article and a second and a	NM_004275	1.34
Consumes includes at ALONS443.1. (DEF = Home septems mRNx: ADIX DIX 225.566/2020 (from clone DIX 225.566/2020). (FEX=mRNX //D8_2X8FF=gr.45.00224 //J6=Hs.161283 Home septems ALONS443	A.049443	<u>.</u>
des finger protein 144 (pHZ-S2)	NM_021964	Ĭ.
ext, even-skipped homeo bar homdog 1 (Prasophita) NN_00198	NM_001989	<u>~</u>
Consensus includes go.AUI 47317 FEB=EST FOB_XREF=gi:1100838 FOB_XREF=estxU147317 K10HE=HAMMA1000340 AU=Hi. 287491 Homo sepiens CDNA FU12140 fis. clone MAMM	AU147317	<u> </u>
tissee inhibitor of metalloproteinese 3 (Sortify fundus dystrophy, pseudoinfammatory)	ARSSESS	5
hypobadcai protein RU10094	AM_U1/333	5
Conserves includes gp.A.[04554] (DEF #Human DNA sequence from done 24058 on chromosome bp11,2-q12, contains the 3 part of a gente for a novel protein similar to 1-31AA, close, 34 Acta 5501.	ALM3544	5 2
THE SECOND WAS CONTROL OF THE SECOND OF THE	A370867	2
Approximate protein Articles	XX 006692	7
Consequence process argulated activation of surrounding	A8037599	2
The second secon	NM 002339	Ž
Off-deposit of the first of the	NH_003027	7.7
Production (LU1234	NM_018383	2
server/Quococritical regulated Unitse	NM_005627	<u>.</u>
probain prosphatose 1, regulatory subunit 10	W492873	7
hypothedical protein FLIZ0132	KM_017682	Ž :
phosphoinosidde-3-Lönese, regulatroy subunit, potypeptide 3 (p55, garma)	A-028/85	1
D0727548H2 (23 protein	N671186	7.7
hypodhalical protein	10000	<u> </u>

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MAAAA SA MAAAA		A6063133 A6241785	3 3
defends prouts metabotrois 2		194552	-
synokial sercome. & breakpoint 2		AF257500	Ž
ektaninas		AF097495	7
brotheft anti- BC(4170		VM 024312	2
Inneffected rentain from done 643		8003379	7
heartheist protein 625965		AC002398	~
stratifin		X57348	~
graguency specific beta-1-dycoprotein 1		KM_006905	7
similar to rat integral men		AU158490	<u>.</u>
hypothetical protein RU1	hypothetical protein FL11316	NM_018388	Ž.
nemanged L-myc fusion sequence		NM_012421	<u></u>
chromosome 21 open reading frame 2		N435747	<u>~</u>
spreuty (Drosophile) homolog 4		NM_030964	<u>-</u>
synudein, germs (bread	specific protein 1)	AF010126	7
syntrophia, games 1		NM_018967	Ž
potassion voltassion	NN state and characteristic states and states are states and states and states and states are states and state	002232	.3
		NM 004318	7
MADAGO mas market		AI 031447	-
perfect Back comme subfamily & R		48002325	2
Contraction advantage programs		AF019381	2
		MA COOS SO	
Carporaphimacine Central		1000 M	5
Common (sensus) seems		MA_016074	5 3
Emiropount Section in the section of		7,100	
cyaconome 1 430, sucrem	ryadramy 1434, socialismy into (injectional actions), postpoproc 3	M79462	5 -
Construct before the state	proxymetry wetgrap with the first three for the first three for the first three for an analysis and a content of the first three for an analysis and a content of the first three for an analysis and a content of the first three for an analysis and a content of the first three for an analysis and a content of three for an analysis and a content of three for an analysis and a content of three for a content of thr	4) 096700	5 2
interferable 12 (cristosis	I-managed actions of the state	NH 002190	7
Commences includes dr.M.	Comments profess of AKD01619   DEF Flores series clib A 5110757 fs. close N7283004528, highly similar to Home saziens mBNA for KJAN0477 protein. FEA=mBNA /08 XBEF=oi. AX001619	1619	2
custine nucleatide binding gratein 11	X ( in the latest terms of	004126	7
immenodobulin supertam	lewither-rich repeal	NH_005545	<u>-</u>
bone morphogenetic protein 4		.51	<u></u>
Consensus includes qb:Al	8933904 /FEA.EST (708. XREF eq.5811123 /708. XREF eq. vz. 55405.x1 / (1.0 N.E. = 1 M.A.G. 2.561961 / (1.0 = 1 M.298.)	3904	Ž
Consensus includes gb:AK	Consensus Includes ap-MO2206.1 (DEF Horms superer CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.296683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.29683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:1043336 / OL=H1.29683 Horns superers CDN FU12003 fis, close HEH1B1001537. /FEA=mRN / DB. /IREF=qi:104003 fis, close FU12003 fis, clo	2065	134
solute carrier family 19 (fi	ACOO Action carrier family 19 (folds transporter), member 1	AF004354	Ţ.
cytechnome P450, subtam	polypeptide 4	AF 182273	č
IDAA0101 gene product	8(00	8(005832	ž
Consensus includes gb:JK	piens CDNA FU23601 fis, clone LN615501. FEA=mRNA /DB_XREF=gi:10440343 /UG=Hs.306918 Homo sapiens CDNA FU23601 fis, cl	7254	<u>.</u>
perusisone profiterative a	percelations profiterable activated receptor, gamma NH_C	NM_015869	<u>.</u>
interferon, eights 5		NM_002169	<u>-</u>
integrin, bata 3 (platefet q	integrit, beta 3 (platelet ghycoprotein file, entigen (D61)	A151479	<u> </u>
Consensus Includes gb:AL	13.1 NEFEHomo supiens mRNK, CDNA DKZD43410523 (from clone DKZD43410523). NEA=mRNA NB_XREF=gi:6808127 /U6=Hs.306465 Homo supiens n	7713	3
hypothetical protein FU10142		NH_018008	<u>~</u>
hypothetical protein FU23239		NM_022766	ž
IQAA1117 protein		AB029040	Ž
S-hydrasytyptamine (serotonin) neceptor 1E		NM_000865	1.34
addelive 3 alpha hydraxys		NM_003725	7
Consensus includes git: BF	:J=EST /08_XREF=gi:10821197 /08_XREF=est:7x76c03.x1 /TLONE=IMAGE:3481325 /UG=Hs.323079 Homo sapiens mRNA; cDNA DNF2p564P116 (fn	5539	<u>~</u>
sepercuide d'smutase 3, extracellular		NM_003102	2
N-myc downstream regulated		960900 WN	<u></u>
PyoD tamily inhibitor		NM_005586	<u>.</u>
6X probin		NM_025262	ř.
potmeiotic segregation increased 2-like 8		601/005	<u> </u>
substance people recepto	Analysis of paper Aguarytets cyclass A (stronatriuretic peptide receptor A)	· ·	3 :
Mornogen - Mare 1	OPPINE A CONTRACT OF THE CONTR	NM_00446/	3:
Source are compared		1450	3 5
draft and and and	MENNE TAKKON RECEIVING WORKER, PRESITE)	MT_003084	3 5
OBSERVED IN IGNING AND ENGLISHED CIRCUIT.		10/35/	3 :
CUS Wiplet repeat, RNA binding protein 2		•	3 :
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and it add to form	)		1
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solute carrier family (6 (menocarboxy); acid transcerent member 3	NM_006314	<u> </u>
cult division cycle 25.	M32/3/8	5
hypothetical protein FU11068	42///24	£.
jenctional achesion notecute 2	#16010_FM	<u> </u>
disherelled, dsh homdog 2 (Dracoshila)	612130 EM	.33
Conserves includes at \$55,000 FEA=FET OR 19FF=#11070150 to A 19FF=#1241541 of Artice Hardenson are in the conserve are in the	77400 64	1.33
Consense includes ab AL 1995.3.1 (DEF Ellow suries while that DEF) AL ALL STATES THE CONSENS WITH THE SHAPE	c33 (n Bc669609	1.33
ACTIVITY OF THE STATE OF THE ST	Apiens AL359563	1.33
OK Wilder manner BM hinders constituted	AB011092	1.33
Andrewson Bell Charles and Control of the Control o	N36839	1.33
Symmetric Control of the Control of	AF 182275	1.3
/2 analy passaults state teachers	NM_021943	1.33
	NM_001711	13
SPIRIT INDUCIOS CYCIOTINE AA	NM 002984	=
Errachphonal unit N143	41002572	3 5
hypothetical protein FU20363	NOC.201	3 :
O24 antigen (small cell has carcinoma chaster 4 antigen)	10710 H	£ :
Extra branch of country weight	86327863	E
flaming bornous mending associated and the second	NM_004321	<u></u>
And the state of t	AB011165	1.3
the second strong of production of the second strong control of the second	A1192838	1.33
	86111635	1.33
amended repeat gene deletes in vetocardiofacial syndrome	NK 001670	=
myelin associated glycoprotein		3 :
Conservate includes gb/M070628.1 /0EF=Homo sapiens done 24803 mRNA sequence. IFEA=mRNA /08 XREF=ai:3283895 Al6=Ht 32756 Homo sapiens alone 24803 mRNA sequence.	4507059	3 :
Consesses Includes gb./F04384.1 /0F# Homo septens close ASKined Lab Immunociologia Immunociologi	92907024	3
Conseque Includes 60,M13124 FEAREST OB XIEE ext 169301 Ol XIEE ext 4319M4 41 MONEMACE ASSESS AND 19824 1. 19824	pood Aruassa	<u>.</u>
doublights to the street BIO 459 with conclusion to the street and	from AV131324	£.
Construct includes the IV(7) 25(2) Afficient (III) The IV(1) Construct includes the IV(7) 25(2) Afficient (III) IV(1) Afficient (III) Afficient (III) IV(1) Afficient (III) Af	AF116705	E.
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when the second second in the second	ens n AL137270	1.33
Land of marriage and marriage a	AL039447	1.33
CONTROL OF THE STANDARD GO STANDARD TO FE BROWN TABLES TO FRANCE TO STANDARD T	16=H AB041269	1.33
Zi no zawana	NM_023067	1.33
protein fyraeine phosphalase, non-receptor type 21	X79510	2
secretory pathway component Sec316-1	AF274863	=
cacherin, Est LNs seven-pars 6-type receptor 2 (famingo homolog, Drosophila)	NM 001408	<u> </u>
hypothetical protein FU22127	AA203219	3 5
host cell factor ?	NW O13320	? :
S-hydranytypLanina (serotonia) raceptor 6	AF007141	3 :
glutamite receptor, metabotropic 1	131216	3 5
Indian hadgahag homalog (Drasophila)	BEBC0473	3 5
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nutita metaloproteinuse 16 (membrane-inserted)	NM 022564	3 5
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estrementar media protein 2, termée organ and adipocyte specific	KM 001393	2
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glacomidates, sight, and (Pompe disease, glycogen storage disease type II)	NH_000152	E.
zinc finger protein RIVZF	NM_023929	=
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ets verlant gone 6 (TEI oncogene)	NM_001987	<u>.</u>
IAB13, member RAS ancagens family	NM_002870	1.33
zárc finger protein 278	AF254087	1.33
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gi:5596067 / OB_XREF = est=m91110:11 / CLONE = IMAGE:2443339 / NG=Hs, 119839 ESTs  done 24566 mRNA sequence. / FEA=mRNA / OB_XREF=gi:3337893 / NG=Hs, 133342 Homo sapiens done 24566 mRNA sequence  14 (BRAN)  14 (BRAN)  15 done (CA01963, /FEA=mRNA / DB_XREF=gi:10437366 / NG=Hs, 287657 Homo sapiens cONX FU21291 fs, chemples despendention)	A899993 A743999 A743999 A8910614 A8910614 A152732 A115733 A11573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A17573 A
1-dependent 3  dane 24566 mRNM sequence. FEA=mRNM /DB_XNEF=gi:3387893 /UG=H±.133342 Hamo stapiens clone 24566 mRNM sequence.  14 (BRAN)  14 (BRAN)  15 (BRAN)  16 (BRAN)  17 (BRAN)  18 (BRAN)  19 (BRAN)  19 (BRAN)  19 (BRAN)	HM_006574 A/41090 A/41090 A/41090 A/41090 A/41090 A/115403 A/115403 A/115403 A/115403 A/115403 A/115403 A/110144 B/004614 Z97053 HW_001555
-dependent 3  done 24566 mRNA sequence. FEA=mRNA /DB_XRF=gi:3387893 /U6=Hs.133342 Homo sapiens done 24566 mRNA sequence  14 (BAAN)  14 (BAAN)  15 (BAAN)  16 (BAAN)  17 (BAAN)  18 (BAAN)  19 (BAAN)  19 (BAAN)  19 (BAAN)	A743090 A9430614 MY_002172 MY_002172 MY_15403 A2 151753 MY_001144 BE044614 BE044614 BE04655 MY_00353
-dependent 3  done 24566 mRNA sequence. (FEA=mRNA /DB_XREF=gi:3337893 /U6=Hs.133342 Homo sapiens done 24566 mRNA sequence  14 (BRAN)  14 (BRAN)  15 done (CAO1963. /FEA=mRNA /DB_XREF=gi:10437366 /U6=Hs.287657 Homo sapiens cONA FU21291 fs. cherinal despendention)	AA910614 NN_002172 NN_002133 AL11543 AL121753 NN_001144 BE044614 SE044614 NN_001533 NN_0015192
-dependent 3  done 24566 mRtW sequence. /FEA=mRtW, /DB_XREF=gi:3337893 /UG=Hs.133342 Homo stpiens clone 24566 mRtW sequence  14 (BRAN)  19 (BRAN)  19 (BRAN)  10 (BRAN)  10 (BRAN)	NN_002172 NN_020393 AL115403 AL121753 NN_001144 BE044614 297053 NN_0012192
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1-dependent 3  done 24566 mRIVA sequence. IF EA=mRIVA /DB_XTEF=gi:3387893 /UG=Hs.133342 Homo sapiens clone 24566 mRIVA sequence  14 (BRAX)  14 (BRAX)  14 (BRAX)  15 (291 fs., done COLO1963. IF EA=mRIVA /DB_XREF=gi:10437366 /UG=Hs.287657 Homo sapiens cDNA: FUZ1291 fs., chemical despenention)	A 115403 AL121753 NM_001144 BE044614 297033 NM_004555 NM_012192
-dependen! 3  done 24566 miltN sequence. /FEA=miltN /DB_XREF=gi:3387893 /UG=Hs.133342 Homo sapiens clane 24566 miltNs sequence  14 (BIAN)  14 (BIAN)  15 (BIAN)  16 (BIAN)  17 (BIAN)	AL121753 NM_001144 BE044614 297053 NM_004555 NM_012192
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done 24566 mRNN sequence. <i>IFEA</i> =mRNA /DB_XREF=gi:3387893 /UG=H1.133342 Homo supiens clone 24566 mRNA sequence 14 (BRAN) 14 (BRAN) 14 (BRAN) 14 (BRAN) 14 (BRAN) 14 (BRAN) 14 (BRAN) 16 (CLO1963 /FEA=mRNA /DB_XREF=gi:10437366 /UG=H4.287657 Homo supiens cDNK FU21291 fs, clerenial despeneration)	NM_005875
done 24566 mRINA sequence.  FEA=mRINA /OB_XTEF=gi:3387893 /UG=Hs.133342 Homo sspiens clone 24566 mRINA sequence 	NM_005567
done 24566 mitht sequence. /FEA=mitht /OB_XREF=gi:3387893 /UG=H4.133342 Homo sapiens clone 24566 mithts sequence  14 (BRAN)  19 (BRAN)	AC136632 RF551361
14 (BAN) 1904. FUZ1291 fis, chore (CA.01963, /FEA=mBNA /DB_XREF=gi:10437366 /NE=Hs,287657 Homo sapiens cDNA: FUZ1291 fis, c	AF070536
14 (BAJA) 19Wi-FUZ1291 fs., clone (CLO1963, <i>FE</i> JamPNA /DB_VREF=g:104171366 /JG=Hs.287657 Homo sapiens cDNk.FUZ1291 fs., cd retinal degeneration)	80004154
14 (BRAX) :ONK: FUZ1291 fs., clone COL01963. <i>JFEA=mRNA f08_X</i> REF=gi:10437366 /JG=Hs.287657 Homo sapiens cONK: FUZ1291 fs., ck retinal despeneration)	131792
14 (BRAX) :DNA: FUZ1291 fs., clone (CQ.01963, <i>FEA=mRNA, DB_XREF=gi:</i> 10437366 /JG=Hs.287657 Homo sapiens cDNA: FUZ1291 fs., c retinal degeneration)	KM_013437
14 (BRA)) :DNK. FUZ1291 fs., chone COL01963. /FEA=mBNK./DB_XREF=gi:10437366 /JK=Hs.287657 Homo sapiens cDNK. FUZ1291 fs. ct retinal degeneration)	MM_001345
14 (BIAN) :DNK FUZ1291 fs., clone COL01963. /FEA=mRNK /DB_XREF=gi:10437366 /VG=Hs.287657 Homo sapiens cDNK FUZ1291 fs., ck retinal degeneration)	NM 001971
(DNV: FUZ1291 fs., clone (OL01963, <i>FEX=mRN</i> A /DB_XREF=gi:10437366 /UG=Hs.287657 Homo sapiens cDNX: FUZ1291 fs., cl retinal degeneration)	NH_004887
ONA. FU21291 fs., done (OL01963. <i>FEA=mRNA (</i> DB_XREF=g:10437366 /VE=Hs.287657 Homo sapiens cONA. FU21291 fs., cl. retinal desperiention)	NM_001208
:DNK. FUZ1291 fs., clone COL01963. /FEA=mRNA /DB_XREF=g:10437366 /UG=Hs.287657 Hamo sapiens cDNK. FUZ1291 fs., cl. retinal degeneration)	039657
. doN. FUZ1231 fs., done (OL01963. /FEA=mRNA /DB_XREF=g:10437366 /NG=Hs.287657 Homo sapiens cONA. FUZ1291 fs., d. refinal degeneration)	NM_022907
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	putable horsectormin transcription factor 1	NM 006608	2
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	c househouse control of	KM_005418	1.30
	Pypopulate protein U 14050	NM_024869	1.30
	Putch "Lancezo	NM_001890	1.30
	probations (protoms, martipain) 265 subunit, ATP 25e, 4	AC007842	1.30
	histofine decerborylase	NM_002112	1.30
	zinc (from ordein 81 (M7220)	168011	1 30
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	SIAI INDICATO SIAI INDICATO SI	NM_004232	.30
	solvite carrier family \$ (socken/liydrogen cachanger), isoform 5	NH_004594	0.30
	prostgandn (2 (prostacycin) synthase	038145	1.30
	zinc fingur protein 154 (pHZ-92)	020648	1.30
	brack/dokn receptor 82	NH_000623	1.30
	Consumos includes go: 86236351 /FEA=EST /08 , XREF = gi: 12750199 /08 , XREF = estimat26112.11 / CLONE=INAGE: 4142350 /US=Hs. 148161 ESTs	86236351	1.30
	eneck At	80000182	1,30
	TNP RNA polymerze II, TATA baz binding protein (TBP)-essociated tector, 150 kD	AK001618	1.30
	colleder retinole acid binding protein 1	NM_004378	1.30
	Exposizomentare (DMA) I	103250	1.30
	sin Associated polypopda, 30t0	NM_003864	1.30
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	cospee recultment domain family, member 15	NH 022162	1.30
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	solves carler family 7 (cationic annino actd transporter, v+ system), member 2	NM 003046	1.30
	hypothetical protein FU20051	NM 019087	1.30
	ACO for serfine protease homologue	AF243527	1,30
	nauropopobol 7 receptor 72	U36269	1.30
	Consumes biduotes gb.AW574818 FEA=E5T /08_XREF = gi.7246357 /08_XREF = ei:U1-HF-8K0-abi-e-06-0-U1.s1 /CLOME=1MAE:305362 /U1G=Hs.32374 E5Ts, Weakly similar to KIAA1528 AW574818	AW574818	5.3
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	hypothetical protein FU10698	AL050219	1.30
	IGAN199 protein	A8033025	1.30
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# 18 / 22209 fb., done HKO1 496, /F.E.F.=mRM / DB_JREF=gi:10438505 / JuE=Hs.285828 Homo supiens cDNA FLUZZZO9 fb., d. 22209 fb., done HKO1 496, /F.E.F.=mRM / DB_JREF=gi:10438505 / JuE=Hs.285828 Homo supiens cDNA FLI4312 fb., clone PLACE31 in 7 DB_JREF=et:17324011.11 / CLONE=HMAE:3248150 / JuE=Hs.287631 serine (or cysteine) proteinsus inhibitor, clade 8 JuE=et:17324011.11 / CLONE=HMAE:3248150 / JuE=Hs.287631 serine (or cysteine) proteinsus inhibitor, clade 8 JuE=et:17324011.11 / CLONE=HMAE:3248150 / JuE=Hs.287631 serine (or cysteine) proteinsus inhibitor, clade 8 JuE=et:1732401.11 / CLONE=HMAE:3248150 / JuE=Hs.287633 Homo supiens inhibitor, clade 8 JuE=et:17324004.6. FEA=mRM / DB_JREF=et:174240011.11 / CLONE=HMAE:31446 / JuE=gi:1043353 / JuE=gi:4500086 / JuE=Hs.287636 Homo supiens cDNA FLI4319 fb. A JuE=et:1740-0411.11 / CLONE=HMAE:3144662 / JuE=Hs.287636 Homo supiens cDNA FLI4319 fb. A JuE=et:1740-0411.11 / CLONE=HMAE:3144662 / JuE=Hs.287636 Homo supiens cDNA FLI2219 fb. A JuE=et:1740-0411.11 / CLONE=HMAE:3144662 / JuE=Hs.287506 Homo supiens cDNA FLI22196 fb. ck v. N. 78, clone HAMHAIO01397. FEA=mRM / DB_JREF=gi:10433318 / JuE=Hs.287506 Homo supiens cDNA FLI22196 fb. ck v. N. N. M.	2000-00-00-00-00-00-00-00-00-00-00-00-00
16.12.6.3)  18.12.6.3)  18.12.6.3)  18.12.6.3)  18.12.6.3)  18.12.6.3)  18.12.6.3)  18.12.6.3)  19.12.6.3)  10.13.	42055 17124 17124 17128 17128 17128 17128 17128 17128 17128 17128 171494 17191 17191 17191 17191 17191 17191 17191 17191 17191
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Trepresent transcript regions 5 prime, Hiddle, and 3 prime respectively)  I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  I Robe, 2008 - 2008	2.866 2.866 993 311.2.8 311.2.8 311.2.8 311.2.8 311.2.8 311.2.8 311.2.8 311.2.8 311.4.
I represent transcript regions 5 prime, Middle, and 3 prime respectively)  17.08_MEF=est.30114312 fs, clone PLACE300322 Alfa Hb. 297681 serine (or orsteine) proteinsse inhibitor, clade (or orsteine) proteinsse (orsteine) prot	22862 22862 311228 2001486 001486 001653 001653 001633 001177 11551 11551 11551 11551
I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  9. 70B_XREF=est:XMI 58566 XCLONE=PLXE3000322 XUE=Hs_257681 serine (or g-steine) proteinase inhibitor, clade 8  9. 70B_XREF=est:XMI 58566 XCLONE=PLXE3000322 XUE=Hs_257681 serine (or g-steine) proteinase inhibitor, clade 8  1. 70B_XREF=est:XMI CLONE=INAGE:2691446 AVG=Hs_256398 Homo supiens mRNX: CDNA DXT26-3450528 (s. p. 108_XREF=est:XMI AVG)  1. 70B_XREF=est:XMI CLONE=INAGE:1738029 AVG=Hs_126398 Homo supiens mRNX: CDNA DXT26-3450528 (s. p. 108_XREF=est:XMI AVG)  1. 70B_XREF=est:XMI CLONE=INAGE:1738029 AVG=Hs_126291 phosphodiesterase 10A FL=gb:AF127491 gb:AF10 AVG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_333540 ESTs, Weably similar to di309K20.4 H.aupiens mBl AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_333678 AVG=Hs_287506 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_333678 AVG=Hs_287506 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_333678 AVG=Hs_287506 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_287506 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_330630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:3434062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:344062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:344062 AVG=Hs_33318 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)  1. 70B_XREF=est:XMI CLONE=INAGE:344062 AVG=Hs_33118 AVG=Hs_30630 Homo supiens CDNA FU12247 AMG)	11228 001486 001486 010533 002538 004306 004306 004177 105 101751
I represent transcript regions 5 prime, Hiddle, and 3 prime respectively)  7. DB_XREF=est:2424-01.s1 / KLONE=PLXE300322 / MG=Hs_225635 Homo sapiens oDNA FU14312 fs, clone PLXES 19 oDB_XREF=est:2424-01.s1 / KLONE=IMAGE3248160 / MG=Hs_236398 Homo sapiens oDNA FU14312 fs, clone PLXES 19 oB_XREF=est:2424-01.s1 / KLONE=IMAGE2631446 / MG=Hs_236398 Homo sapiens mRNX CDNA DWZp434C0328 (A A A A A A A A A A A A A A A A A A A	201468 201468 1830 202658 204306 2014945 201117 11540 11346 11351
I represent transcript regions 5 prime, Middle, and 3 prime respectively)  7.08_XREF=ext.XII 58566 ACLONE=PLAE3000322 ACE=H3.297681 serine (or orsteine) proteinsse inhibitor, clade 89 ACLONE=HMAE3248150 ACE=H3.297681 serine (or orsteine) proteinsse inhibitor, clade 89 ACLONE=HMAE22691446 AUG=H3.295898 Home supiens cDNA PU14312 fs., clone PLAE319 ACCES ACLONE=HMAE22691446 AUG=H3.295898 Home supiens mRtw. cDNA DNF2p434E0528 (s. Acces PLAE3000406. ACLONE=HMAE22691446 AUG=H3.256398 Home supiens mRtw. cDNA DNF2p434E0528 (s. Acces PLAE31900406. ACLONE=HMAE22691446 AUG=H3.26291 phosphodiesterase 10A ACL=gp.AF1234319 fs. Acces ACLONE=extraceOut11.x1 ACLONE=HMAE239329 AGE=H3.128291 phosphodiesterase 10A ACL=gp.AF123491 gs.). ACLONE=HMAE33434062 AUG=H3.33540 EST1, Weasky similar to di309ACO.4 H.supiens mRt MAN ACLONE=extraceOut12.x1 ACLONE=HMAE33434062 AUG=H3.33540 EST1, Weasky similar to di309ACO.4 H.supiens mRt MAN ACLONE ACCORDANCE ACCES ACCORDANCE ACLONE ACCES ACCORDANCE ACCES ACCORDANCE ACCES ACCORDANCE ACCES ACCORDANCE ACCES ACCES ACCORDANCE ACCES	201430 1016053 0002638 004306 004306 00117 13460 13450 13451
7.08_XREF=est.3u1 545-66 ACLONE=PLACE3000322 ALG=H3.237635 Homo sapiens o'DNA FU14312 fs., clone PLACE31 of AB_XREF=est:7024-01.s1 ACLONE=PLACE30232 ALG=H3.237681 serine (or systeine) proteinase inhibitor, clade in the control of AB_XREF=est:7024-01.s1 ACLONE=IMAGE.2891446 ALG=H3.256398 Homo sapiens mRNA; CDNA DNE7243460228 (s. A.	01553 002638 004306 001117 1105 13460 01333
17 // DB_XREF=ert:WII 58566 // LONE=PLACE300322 / VIG=Hs_287635 Homo sapiens cDNA FU14312 fs, clone PLACE31 is 10 // DB_XREF=ert:7424-c01_x1 // CLONE=IMAGE3248160 // VIG=Hs_287635 Homo sapiens cDNA FU14312 fs, clone PLACE31 // CDB_XREF=ert:m9040.08.x1 // CLONE=IMAGE2691446 // VIG=Hs_286398 Homo sapiens mRNX cDNA DWZp434C9328 (s A red factor, 31 tb)  DB_XREF=ert:q=c0411_x1 // CLONE=IMAGE:1738029 // VIG=Hs_128291 phosphodiesterase 10A // FL=gb.XF 123491 gb.XF no sapiens cDNA FU14319 fs, and sapiens cDNA FU12247 Ms, and sapiens cDNA FU22396 fs, and sapiens cDNA FU	.010033 000538 00106 0114945 001117 105 115 11551 013435
17.70B_JREF=ert.JUI: 545-66 /TLONE=IMAGE:3245160 /LG=Hs.237631 serine (or cysteine) proteinsse inhibitor, clade 19.70B_JREF=ert:7424-601.s1 /TLONE=IMAGE:3245160 /LG=Hs.237651 serine (or cysteine) proteinsse inhibitor, clade 19.70B_JREF=ert:m90u-01.s1 /TLONE=IMAGE:2691446 /LG=Hs.256398 Homo supiens mRNA; cDNA DK72p434c50528 (s. 2019) with the contemporal contempora	.004306 .004306 .001117 .005 .13460 .17551
7.08_XREF=est;X24-C01.s1 (XLONE=IMAGE:3248160 XIG=H3.237635 Homo supiens obtok FU14312 fs, clone PUKE31 (108_XREF=est;X24-C01.s1 (XLONE=IMAGE:3248160 XIG=H3.237681 serine (or cysteine) proteinase inhibitor, clade 19.08_XREF=est;X24-C01.s1 (XLONE=IMAGE:2691446 XIG=H3.256398 Homo supiens mRNA; CDNA DU72p4346028 (s. 18.28) fs, clone PUKE3000406. FEA=mRNA /DB_XREF=g;10436753 XIG=H3.287636 Homo supiens cDNA FU14319 fs, A red factor, 31 kD A red factor, 32 kD A red factor, 31 kD A red factor, 32 kD A red fa	.044945 .041945 .001117 105 13460 17551 013435
17 / DB_XREF=eet-MISSSG6 / CLONE=PLACE3000322 / MG=Hs_287635 Homo supiens cDNA FUI 4312 fs, clone PLACE31	.014945 .001117 105 13460 17551 013435
17 / DB_XREF=ert:WI 158566 / CLONE=PLACE3000322 / MG=Hs_297681 serine (or cysteins) proteinsse inhibitor, clade of the control of the control of cysteins of the clade of the control of the clade	,001117 105 13460 17551 013435
17 // DB_XREF=eet; WI 18856 // LONE=PLACE3000322 / ALG=H3_237635 Homo sapiens cDNJ FU14312 fs., clone PLACE31  9 // DB_XREF=eet; A224c01_s1 // CLONE=IMAGE:2248160 // A16=H3_256338 Homo sapiens mRNA; cDNJ DNZ-P434C0528 (p. 1708_XREF=eet; A224c01_s1 // CLONE=IMAGE:224160 // A16=H3_256338 Homo sapiens mRNA; cDNJ DNZ-P434C0528 (p. 1808_XREF=eet; A226300406. // FEA=MRNA // DB_XREF=gi:10436753 // A16=H3_256338 Homo sapiens cDNJ FU14319 fs. A A A A CONE_CONE_CONE_CONE_CONE_CONE_CONE_CONE_	105 13460 17551 013435
17 / 78_ JAEF = est. JAZ 4-01.1 / KLONE = IMAGE:3246160 / 1/6 = 143.297631 serine (or cysteine) proteinase inhibitor, clade 19 / 708_ JAEF = est. JAZ 4-01.1 / KLONE = IMAGE:3246160 / 1/6 = 143.297631 serine (or cysteine) proteinase inhibitor, clade 19 / 708_ JAEF = est. JAZ 4-01.1 / KLONE = IMAGE:2691446 / 1/6 = 143.265938   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 143.287636   1/6 = 1	13460 17551 013435
7.08_306F=est;3014.016.016.016.016.016.016.016.016.016.016	17551 013435
17 / OB_XREF=est: XISSG6 / CLONE=PLACE300322 / VG=Hs.297631 serine (or cystems) proteinase inhibitor, clade (or cystems) clade (or cys	013435
17 / 70 B_XREF=est:XWI 58366 / KLONE=PLACE3000322 / JuG=H3.297681 serine (or cysteine) proteinase inhibitor, clade to the control of the cont	
17 / 708_XREF=eet12M24401.11 / TLONE=INAGE:3248160 / 16=14.287651 kmm sapiens GNUs FUL14312 fs, clone PUACE31  9 / 708_XREF=eet12M24401.11 / TLONE=INAGE:2248160 / 16=14.285398 Home sapiens mRNA; cDNA DAFZp434E0528 (p. 168_XREF=eet12M20406.11 / TLONE=INAGE:2291446 / 16=14.285398 Home sapiens mRNA; cDNA DAFZp434E0528 (p. 168_XREF=eet12M20406.11 / TLONE=INAGE:1738029 / 16=14.128291 phosphodiesterase 10A / FL=gb/AF1274/9.1 gb / 108_XREF=eet12M20781 / FEA=mRNA / 708_XREF=ej:4500086 / 10=14.21103 Home sapiens mRN A / 108_XREF=eet12M20781 / FEA=mRNA / 708_XREF=ej:4500086 / 10=14.21103 Home sapiens mRN A / 108_XREF=eet12M20781 / FEA=mRNA / 708_XREF=gj:10433678 / 10=14.21505 Home sapiens cDNA FU12247 / 108_XREF=eet12M2044 / FEA=mRNA / 708_XREF=gj:10433678 / 10=14.287506 Home sapiens cDNA FU12247 / 109_XREF=gj:10433918 / 106=14.287506 Home sapiens cDNA FU12247 / 109_XREF=gj:10439318 / 106=14.330680 Home sapiens cDNA FU12247 / 109_XREF=gj:10439318 / 106=14.306850 Home sapiens cDNA FU12247 / 108_XREF=gj:10439318 / 106=14.306850 Home sapiens cDNA FU12247 / 108_XREF_gj:10439318 / 106_XREF_gj:10439318 / 106_XREF_gj:10439318 / 106_XREF_gj:10439318 / 106_XREF_gj:10439318 / 106_XREF_gj:10439400000000	003770
9 / 708_XREF=ext:xm90u08.11 / KLONE=INAGE:3248160 / 1/6=H3.297681 serine (or cysteine) proteinase inhibitor, clade in / 708_XREF=ext:xm90u08.11 / KLONE=INAGE:2691446 / 1/6=H3.256398 Homo supiens mRNA; cDNA DK72p434E0528 (h. 1/2012) to 1/2012 / 201	58566
(**) DB_XREF=ext:rm90u08.11 /CLONE=IMAGE:2691446 /VG=H4.256398 Homo sapiens mRNV; CDNA DVFZp434E0528 (h. 1319 fs., clone PLACE3000406. /FEA=mRNA /DB_XREF=gi:10436753 /VG=H3.287636 Homo sapiens CDNA FU14319 fs. 2014 fs. 2014 fs.) and the control of the control o	72818
119 ft, clone PLACE3000408.11 ALONE=INACE.2691446 AVG=Hs.256398 Homo supiens mRNA; CDNA DXT2p434E0528 (s. 18. 200. AREF=estim-90408.11 ALONE=INACE.2691446 AVG=Hs.256398 Homo supiens cDNA FU14319 ft. 1 ted textor; 31 tb. 1 to the process of the pr	183100
(**) ** ** ** ** ** ** ** ** ** ** ** **	96630
13 6 fs, clone PLACE3000406. /FEA=mRNA./08_XREF=gi:10436753 /UC=Hs.280636 Homo supiens cDNA FU14319 fs. led factor, 31 tb  OB_XREF=est:qeCM11.c1 /CLONE=IMAGE:1738029 /UG=Hs.128291 phosphodiesterase 10A /FL=gb-AF127479.1 gb J R P COTZ-65648076 (from clone DIGZ-65648076) /FEA=mRNA./08_XREF=gi:4500086 /UG=Hs.21103 Homo supiens mR A A A A A COTZ-65648076 (from clone DIGZ-65648076) /FEA=mRNA./08_XREF=gi:10433678 /UG=Hs.287506 Homo supiens cDNA FU12247 A A A A A A A A A A A A A A A A A A A	588510
i. OB_JREF=estim90408.11 KLONE=INAGE:2691446 AUG=H4.256398 Homo sapiens mRNV: CDNA DNETp434E0528 (h. 1918) file of the CDNA DNETP434E0528 (h. 1918) file of the CDNA DNETP434E0528 (h. 1918) file of the CDNA DNETP434 GOAR PLOSE OF THE CONTROL OF TH	9,4
119 fs. clone PLVE3000406. FEb=mRNA /DB_XREF=gi:10436753 /UG=Hs. 287636 Homo sapiens cDNA FLI14319 ft. 108_XREF=est;qcO411_x1 /CLONE= NAGE:1738029 /UG=Hs.128291 phosphocitesterase 10A /FL=gbs/61274/9.1 gbs/ 108_ZXEF=est;qcO411_x1 /CLONE= NAGE:1738029 /UG=Hs.128291 phosphocitesterase 10A /FL=gbs/61274/9.1 gbs/ 108_XREF=est;nac01b12_x1 /CLONE= NAGE:3434062 /UG=Hs.33540 ES1s, Weakly similar to di309120_4 Hs.apiens mR1 108_XREF=est;nac01b12_x1 /CLONE= NAGE:3434062 /UG=Hs.33540 ES1s, Weakly similar to di309120_4 Hs.apiens PN 108_XREF=est;nac01b12_x1 /CLONE= NAGE:3434062 /UG=Hs.33540 ES1s, Weakly similar to di309120_4 Hs.apiens PN 108_XREF=est;nac01b12_x1 /CLONE= NAGE:3434062 /UG=Hs.33540 ES1s, Weakly similar to di309120_4 Hs.apiens PN 108_XREF=est;nac01b12_x1 /CLONE= NAGE:343638 /UG=Hs.306850 Homo sapiens cDNA FLIZZZ37 in Record MANHALIO01397 /CLONE WANAZ344 /FEA=mRNA /DB_XREF=gi:10439318 /UG=Hs.306850 Homo sapiens cDNA FLIZZZ396 fs. ct A A A	. 1022
319 fs, clone PLACE3000406. /FEA=mRNA /DB_JREF=gi:10436753 /UC=Hs, 227636 Homo sapiens CDNA FU14319 fi. ted textor, 31 tD  OB_JREF=est:qeCuti1.x1 /CLONE=IMAGE:1738029 /UC=Hs.128291 phosphodiesterase 10A /FL=gb:A127479.1 gb.J  LOGZpS648076 (from clone DNGZpS648076). /FEA=mRNA /DB_JREF=gi:4500086 /UC=Hs, 21103 Homo sapiens m81 /DB_JREF=est:nae()1b12.x1 /CLONE=IMAGE:3434062 /UC=Hs, 333340 ESTs, Weakly similar to di309N20.4 H sapiens 10A fb1, clone MANHA1001397. /FEA=mRNA /DB_JREF=gi:10433678 /UC=Hs, 287506 Homo sapiens CDNA FU12247 st. As As fbs, clone MANHA1001397. /FEA=mRNA /DB_JREF=gi:10433918 /UC=Hs, 306850 Homo sapiens CDNA FU12247 st. As As As clone MANHA1001397. /FEA=mRNA /DB_JREF=gi:10439318 /UC=Hs, 306850 Homo sapiens CDNA FU122796 fs, ct.A. As As an example of the clone for the clone for the clone frame for the clone for the clone frame for the clone for the clone frame for the clone frame for the clone for the clone frame for the clone for the cl	2343
139 St., clone PLACE3000406. /FELS=mRNA. /DB_JREF=gi:10436753 /NG=Hz.287636 Homo sapiens cDNA FLJ14319 fi.  106_JREF=extrac-0411.x1 /CLONE=INAGE:1738029 /JG=Hz.128291 phosphodiesterase 10A /FL=gb:M-12749.1 gb:J  106_LREF=extrac-0411.x1 /CLONE=INAGE:1738029 /JG=Hz.32591 phosphodiesterase 10A /FL=gb:M-12749.1 gb:J  106_LREF=extrac-0411.x1 /CLONE=INAGE:3434062 /JG=Hz.33540 E51z, Weakly similar to di309/20.4 H sapiens RR1  127 fs, clone MAHHA1001397. /FEA=mRNA /DB_JREF=gi:1043678 /JG=Hz.287506 Homo sapiens cDNA FLJ2247 is RR1  136 fs, clone KAUZ544. /FEA=mRNA /DB_JREF=gi:10439318 /JG=Hz.306650 Homo sapiens cDNA FLJ2247 is RR1  137 fs, clone KAUZ544. /FEA=mRNA /DB_JREF=gi:10439318 /JG=Hz.306650 Homo sapiens cDNA FLJ2247 is RR1	92
119 fs, clone PLAESOCOAGO, FELA-MRNA / DB_XREF-g;:10436723 /U/C=H;, 28/636 Homo sapiens cDNA FU14319 fs, tone tacker, 31 tD  DB_XREF=est;qcO4111.11 /CLONE=INAGE:1738029 /U/C=H;, 128291 phosphodiesterae 10A /FL=gbx/F1274/9.1 gbx)  OB_XREF=est;qcO4111.11 /CLONE=INAGE:1738029 /U/C=H;, 33540 E51;, Weaky similar to di309/20,4 H; sapiens mlt in the control of the contro	1813
red factor, 31 kD  OB_XREF = extractOHII.rI /CLONE=IMAGE:1738029 /VG=H3.128291 phosphodiesterase 10A /FL=gb:/V127479.1 gb.)  OB_ZREF = extractOHII.rI /CLONE=IMAGE:1738029 /VG=H3.128291 phosphodiesterase 10A /FL=gb:/V127479.1 gb.)  OB_ZREF = extractOHII.rI /CLONE=IMAGE:3434062 /VG=H3.33540 ESTs, Weakly similar to di3099/20.4 H sapiens RNI)  AP fis, chone MAMHA1001397. /FEA=IMINA /DB_XREF = gi:10433678 /VG=H3.306850 Homo sapiens CDNA FLI12247 Is  NOTE TO SET IN THE SET I	4381
09_XREF=eritqCdf11.x1 /CLONE=IMAGE:1738029 /V6=Hx.128291 phosphodiesterase 10A /FL=gbx/F1274/9.1 gby, CD/ZpSc48076 (from clone DRF2pSc48076), /FEA=mRNA /DB_XREF=gr.4500086 /UC=Hx.21103 Homo sapiens mR1 /DB_XREF=eritnae01b12.x1 /CLONE=IMAGE:3434062 /UC=Hs.33540 ES11, Weakly similar to di309K20.4 H sapiens mR1 / Link /CLONE=IMAGE:3434062 /UC=Hs.335340 ES11, Weakly similar to di309K20.4 H sapiens mR1 / Link /CLONE IMAGE:3434062 /UC=Hs.33578 /UC=Hs.287506 Homo sapiens cDNA FU122471 is / Link /CLONE KUNZS44. /FEA=mRNA /DB_XREF=gi:10439318 /UC=Hs.306850 Homo sapiens cDNA FU122471 is / RA / RA / Link /CLONE KUNZS44. /FEA=mRNA /DB_XREF=gi:10439318 /UC=Hs.306850 Homo sapiens cDNA FU122471 is / RA / R	6050
OB_JREF=estracOdf11.s1 KLONE=IMAGE:1738029 /U6=Hs.128291 phrosphodiesterase 10A FL=gb.XF127479 1 gb.y  ODFZ\$5548076 (from clone DRF\$5548076), FEb=mRNA /D8_JREF=gi-4500066 /U6=Hs.21103 Homo sapiens mR1  /D8_JREF=estracOlb12.s1 /KLONE=IMAGE:3434062 /U6=Hs.33540 E515, Weakly similar to di309120.4 H sapiens mR1  (47 fs, clone MAMMA1001397, FEA=mRNA /D8_JREF=gi:10433678 /U6=Hs.287506 Homo sapiens cDNA FU12247 (7)  196 fs, clone KANA2544, FEA=mRNA /D8_JREF=gi:10433318 /U6=Hs.306850 Homo sapiens cDNA FU122796 fs, ck ///  197	130927
1067255648076 (from done DG7255648076), FEX=m8141, NB_XREF=gi-4500086 /NG=Hs, 21103 Homo sapiens mRI  ** // // // // // // // // // // // // /	879
ODGZQ5648076 (from clone DDGZQ5648078), FEL=mRNJ, OB_JREF=g;-4500066 /UG=Hs.21103 Homo sapiens mRl  OB_JREF=estinae01b12.s1 /KLONE=IMJGE:3434062 /UG=Hs.33540 E51s, Weably similar to di3091k20.4 H sapiens  147 fs, clone MAHHA1001397, FEL=mRNJ /DB_JREF=g;10433678 /UG=Hs.287506 Homo sapiens cDNA FLJ1224711  158 fs, clone KAUA2544, FEA=mRNJ /DB_JREF=g;10439318 /UG=Hs.306850 Homo sapiens cDNA FLJ1224711	1637
ODG_DSG48076 (from clone DDG_DSG48076), FEN=mRIA, NB_XREF=gi-4500066, NJG=Hs, 21103 Homo sapiens mRI  / NB_XREF=estrace(1b12.s1 /KLONE=IMAGE:3434062 /NG=Hs,33540 E515, Weakly similar to di309N20.4 H sapiens / NB_XREF=estrace(1b12.s1 /KLONE=IMAGE:3434062 /NG=Hs,33540 E515, Weakly similar to di309N20.4 H sapiens / NB_XREF=estrace(1b12.s1 /KLONE=IMAGE:343676 /NG=Hs,287506 Homo sapiens cDNA FU12247 if the clone NANA2544. FEN=mRIA /NB_XREF=gi:10433318 /NG=Hs,306850 Homo sapiens cDNA FU12247 if the clone NANA2544. FEN=mRIA /NB_XREF=gi:10433318 /NG=Hs,306850 Homo sapiens cDNA FU122796 fis, ck /NB	
V. DB_XREF=estrate() b) 2.1 / KLONE=IMAGE:3434662 / AlG=Hs.33540 ESTs, Weaky similar to di309/20.4 H. sapiens  Y. DB_XREF=estrate() b) 2.1 / KLONE=IMAGE:3434662 / AlG=Hs.33540 ESTs, Weaky similar to di309/20.4 H. sapiens  (47 fs, done MAHHA1001397. / FEA=mRNA / DB_XREF=gi:10433678 / NG=Hs.287506 Homo sapiens CDNA FU12247 to 1996 fs, done WANA2344. / FEA=mRNA / DB_XREF=gi:10433318 / AlG=Hs.306850 Homo sapiens CDNA FU122796 fs, do	17971
/ DB_JXEF = cettnac() b) 2.1 / CLONE=IMAGE3434062 / UG=Hs.33540 ESTs, Weably similar to di309K2().4 H. sapiens (47 fs, done MAMMA1001397 , /FEA=mRNA / DB_JXEF=gi:10433678 / NG=Hs.287506 Homo sapiens cDNA FLJ12247 1, (78 fs, done KWAZ544 , /FEA=mRNA / DB_JXEF=gi:10439318 / NG=Hs.306850 Homo sapiens cDNA FLJ12247 1,	9313
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plant this homelene Sta demain tenth & manches !		3
One (Repot) homolog, subfamily C, member 8		•
IDA/0775 sene product	90	4
phospholipae D1, phophoticlydrofme-specific		6
Consense includes gb.4L121975 DEF = Numen DNA sequence from close RP3-422811 on chromosome 6p11.2-12.3 Contains ESTs, STSs and GSSs, Contains part of the PRIM2A gene for Inv AL121975	_	.4
hypothetial protein FU20047	NM_017639 1	9
rethrick and receptor, alpha	_	.4
CONSESSED HOUSE GLAF OD SETTING THE PROPERTY IN THE CHEST II SATISFON (CREED) MINIA, HIA-DRBG 10201 silvets, sequence. If EXI-ENRIVA (DB_XREF=gi:5915893 /UG=Hs, 167385 Homo AF005487		9
erythrosyta membrane protein band 4.1 -the 2	<b>.</b>	<b>Ģ</b>
calcium-sensing neceptor (hypoculicum) typerunicemia 1; severe neonatal hyperparathyroidism)		€.
perfiltro hornolog 1 (Drosophila)		₹.
DNA segment on dreamosoms (unique) 2654 expressed sequence		9
capase II, approposit-related cystems professes	530	÷:
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telomest reseal binding factor (NIIAL-interacting) t	_	4
Conserva includes do # 23837 ( 106 = Home success clone 6.15H 3 similar to diadrin mRNA sequence. / FEAxmRNA //DB XREE = cr. 2272577 //JG = Hs. 275706 Home success clone 6.15H 3. # 2238370		9
doublecortu; Essercehaly, Arinted (doublecortis)		9
metria entallocutainas (3 (collacenses 3)		9
unidate manophosphate synthetise (ordate phosphoribosyt transferase and orotidine-5'-decarbouritase)		9
Consenses includes ob-MOZ4976.1 / DEF Home supplies CON4. FUZ1323 fs. done COL02374. /FEA=#1NA /DB. XXEF=#110437405 /UG=Hs.75914 Home supplies CONA. FUZ1323 fs. done COL02374. /FEA=#1NA /DB. XXEF=#110437405 /UG=Hs.75914 Home supplies CONA. FUZ1323 fs. do XXQ24976	_	9
Comments includes gb.M.D50032.1 (DEF = Hours septems mRNV; cDNA DKT2p566F 1224 (from close DKT2p566F 1224), FEA=mRNA /DB_XREF=gi-4884272 /UG=Hs.306307 Home septems ALD50032	-	4.
protein (peption) de/trans bonnerse) MMA-interacting, 4 (pervulin)		\$
offactory receptor, family 7, subfamily C, member 1	-	\$
thrulling petain ZJRK i	283	₹.
cylectrone P4So, subtamily IA (phenobartrial-inducible), polypeptide 6	-	\$
hypothesis 12 protein FUZOR24	NM_017906	9 1
FIRE marks 116 corrected family		<b>9</b> 4
affectioning living		2 4
conditions where it is the artist and an artist likely orthology of muse CRSO feelbowness recent contains someone of XLADs contains		3 4
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solve caries tank 1 (sodum-dependent increase chrosolvate cotranscorter), member 7		4
Communia includes do: H49077 FELMEST (708 JAEE mai-388918 (708 JAEE metry 18-05, s1 / CLONE = INAGE (274160 / UG=H1, 159179 Homo sapiens mRNA sequence, INAGE (lone 44641)	H49077	. 4
phosphodistrense 40, cAMP-specific (phosphodistense E3 dunce homolog, Drosophilia)	R40917	.46
PLAnothed I homeobox 2	290	<del>4</del> .
parini, apha		.46
bone morphogenetic protein 5		\$
Down syndrome critical region gone 1-like 1		₹.
p00ACP-escodeme factor		9
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Thomas de de la company de la	NW 003235	9
	רכיזראייייי	
guarine medeotide-releasing factor 2 (specific for cit proto-oncogene)	NM_005312	94.1
	86742268	1.46
Trachella Jacken (Wilson C. Commins)	BC005153	34.
potassees charact, suffaciently it member 15 (1884-5)	NM_022358	1.46
Commens removes governor grants and the commens of the commens removed by the commens remov	ALS67940	9
information processing to proceed the process of th	AL022101	9 :
softer carrier family. Cathorise persons and family and the sections in manches 14	/65/10 HW	9
hypothetical protein FLZ3129	NA_014331	9 4
dhonnaone 22 open reading frame 3	AA018187	9 4
hypothetical protein FUZ1276	NM 024633	97
E-MV	NM 004440	2 4
IQMO480 gene product	AW299294	1.46
Consenses includes go.187222483 FEA=EST (AB_XREF=gi:11129660 (AB_XREF=est:7p5340).11 //LONE=IMAEE3849417 /UE=Hs.274454 ESTs, Weakly similar to 2004399A chromosom; BF222483	som: BF222483	46
RDMOAT7 gene product	NM 025015	9
Consenses includes 95:57328.1 / DEF sparcracks ribonuclesse human, mRNA Recombinant Parial, 491 nl. /FEA smRNA //EBH=pancrashs ribonuclesse, MP-Shase //R0D=pancrashs ribonu 579281	xonu 579281	9
Consensus includes go ACMS18.1 /OEF = Homo sequens mRNA, cDNA DIVIZp56411916 (from clone DIVIZp56411916). FEA=mRNA /DB_XREF=gi. 4499947 /UC=Hs. 306291 Homo sequens in AL049218	ns n AL049218	9
hypothetical protein FLR3311	NM_024680	1.46
metry/metronate-emission/ryde dehydrogenase	66399778	3.
transcription factor 7-tile 2 (T-cell specific, RM6-box)	A1270770	1.46
For Imparant of 195, for afficity II, receptor for (CD23A)	NM_002002	1.46
Conservation includes gb-ALGBO161.1 (DEF #Homo septions mRNA, cDNA DIVIZE-434N144 (from clone DIVIZE-434N144). FEA=mRNA /DB_XREF=gi-SE62623 /UG=Hs. 210431 Homo septions	s mi AL030161	1.46
gonadorophi-reaeming hormone receptor	L03380	34.1
MARTIN CONTROLLED	M22094	1.46
CONSTRUCTION OF THE STATE OF TH	BF109941	34.
Market graphone receptor i, cTP banding protein	NM_001716	1.46
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soldes carrier barily 2 (traditional glucose transporter), member 3	AA778684	9
Acting requisit complementating defeatible repair in Oninese hanster cells 2	NM_005431	1.46
s promissource families 6	AF040751	1. 8
The Branche and growth reports	NM_005655	 94.
Caragest response format of the service of the serv	NM_003304	1.46
CARDER SEASON OF THE SEASON OF	BE552409	1.46
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CGL143 protein	NM_016074	3 4
transmittran 4 superfamily member 1	A1346835	1.46
uniconnus	NM_003007	1.46
CONTROL CHARLES, CARLOL BATCH MEMBER 2	NM_006536	1.46
monther manufacture 2.	NM_022122	9.
Generals includes and NNY2339 FELEST (DB XIEF and 162705 AB XIEF and FETTALKS) AIR also sources	811500_MM	÷.
extrin-12	106309	<u> </u>
homo bar R2	UN 002145	9 4
hypothetical protein FU10232	NN 018033	<u> </u>
small inducible cytolice suctionity A ((ys.4ys), member 19	188321	4
GAT tumorigamicity conversion 1	025433	4
hypodhebical protein PR01617	NM 018587	1.46
The state of the s	NM_002031	1.46
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ekatikon Sturesierae M4	M99422	-
150 mm (cooper)	NH_014625	Ξ.
guarantizaid modulatory dement binding protein 2	AL 133646	9
nuclear receptor coactivator 2	AM02/4/4	
eryteropolettin	A-033330	
par-3 partitioning defective 3 homolog (c. elegans)	A 130183	
hippocalcin-like protein 4	NW 002960	3
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despite the foreign contraction of the foreign contract of the foreign contrac	AU276803	-
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Constrone P.S. addrain M. (Inspection - Inspection 8	NM_000770	1.46
hypothetical protein	NA_015370	<b>-</b> :
hypothadical protein RU10260		<b>:</b> :
Conserved includes git.AL137475.1 (DEF =Home sepiens mANA: CDNA DVEZp434F0723 (from done DVEZp434F0723). FEA=mRNA (DB_XREF=gi:6808086 /UG=H3.274578 Home sepiens	saprens AL137475	
reboxomal protein S6 timose, 90t0, polypeptide 5	MM_U04/33	
RAS guaryf releasing protein 2 (saform and DAE-regulated)	NM 004738	4
VAP reside associated members protein Jasociated perfect in 800 to 100 t	NM_015879	34.
THE PROPERTY OF THE PROPERTY O	6001777	<del>-</del>
Improvement 11 count reading frame 25	A300461	-
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Prochability protein FU20126	KM_017677	I :
hance necrosis factor receptor superhamb, member 12 (translocating chain-association membrane protein)	094506	2 4
cations charvel, voltage-dependent, gamma subunit 5	NM_01404	
design in	A1493245	: 2
Clief angent function and inclusion above group system)	NM_016619	-
imponence private. Inducate immandiabilish in recetor, suchtamily A (with TM domain), member 1	NN_006863	2
Consumus includes go.XXX25206. I (DEF=Horno supiers cDNA FUZ1553 fig. clone (OLO6329, /FEA=mRNA /DB_XREF=gi:10437671 /UG=Hs. 306786 Homo supiers cDNA FUZ1553 fig. cl. XXX25206	53 fis, ct AK025206	9.
sishfernorske 8K (sipha2, 3KsDeta 1, 4KkWkalpha 2, Baishfernorskense)	NM_0158/9	÷ +
Suprificeacing complex products	AW593859	4
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order to the second of the sec	HM_000045	-
Consumes Includes at ALOSO391; A DEF ENOTO Supiers millAN, cDIA DIVZDSS6A181 (from done DIVZDSS6A181); partial cds. FEA=mRNA /GEN=DIVZDSS6A181 /PR00=hypothetical pn ALOSO391	etical pr AL050391	-
N.27330 Namen 285 ribasoma RNA gene, complete cds [_S, _H, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	M27830	9.
chr. finger protein 286	X90Z0_WN	<u> </u>
6 entgon 3	NM 006451	2
polyamatak binding poten-mirrancing protein 1	NM_024938	
impositoria potenti I.U. 1503. Immundini A.A. form B.A. Tomoromet of semideid reveniment	86260394	-
systems, target from the company of	AW186198	
cysteine and dychre-did probein 2	046006	<b>:</b> :
phosphaddyfinowitel dycur, class (	NM_002642	<u>.</u>
Chambine Ble receptor 1	2/04/07/14	
Community includes go MEEST (08 ARE = 9:9873045 (08 ARE = estAV552031 ALONE HELLE MAIZ AUGENS 240 FORD 540 FORD	AF152507	- 1
procedured garms source: A. I.	AF220028	-
uniform security (interaction contains)	A1824012	-
meran-bindra lecto series protesse 2	NM_006610	Ξ:
probacytem 4, (magalamycyte stimulating factor, articular superficial zone protein, camptodactyty, arthropathy, cosa vam, perkartitis syndrome)	NM_00580/ AARROS7	<u> </u>
placeping (3 prints) Resulter on 1166-at 12701824 AR 1865-at 130311 KT DRE-ESODDO27R0G (3 prints) AGE-HS.111243 MADS but transcription enhancer facts MS30311	cer facts ALS30331	1.45
CONTRACTOR PROCESS OF THE PARTY	BE895437	-
organisms includes go publicated for Ethomo supiens 5HT3 gene for servicinis 1 receptor FEA=mRNL_2 (AB_JIREF=gi17019744 AUG=Hs.2142 5-hydroxytryptamine (servicinis) receptor : AV005205	eceptor : A005205	\$ :
phospholipase A2 group IID	AL158172	÷.
Consumes includes go.A.1390157.1 / DEF = Homo supiens mRNA: CDNA DNF264340179 (from clone DNF264340179). / FEA=mRNA / DB_XREF = 91:936884 / JUB=H3.3U6>20 Homo supiens m.N.4.301.3V	piens mi ALSSO157	•
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is profusional receptor 56  Call receptor 56  Ca	om channel 1 /DB XREF = 01:9789940 /UG=Hs 283369 NM 019841
Commontor trapport to the common of the comm	AL554008
ementurus protein 5 dodinal diferentiation, hypotosphaide aid 6-protein-coupled receptor, 2 *elaboration (Meta 1,4-gulatosphaide aid prophophide 2 seems includes gobyllistes) / Florie From JATE = gi:11010478 //DB_AREF =est.AU148957 /KLONE = MT2RH4001313 /UE=Hs.30	AW007751
B1655366 B16	BF224146
-Ledwardskikk beta 1,4 gukton/frantieras, polypsytós 2 sensa induka gydullysző J Főleső J AB, "JGE sgi:11010478 //DB_JREF=est-AU148957 /KLONE=MTZRM4001313 /UG=Hs.30 szense főta arcogenestsociánd para	BF055366
<b>Lansansa inclucia go/Uli (4957 /FE/=EST /OB_XREF</b> =gi:10104/8 /OB_XREF=est:/Uli (4957 /CLONE=NIZRN4001313 /UG=Hs.30 Lancapan (Vra ancogana-asociated gans)	BC002431
coapen (Kns oncogene-essociated gane)	06638 Homo sapiens cDNA FU12591 hs, clone N12KM AU146957
	AL130736 NM 006042
reported sensor (government) belongs asserted as in	NW_005775
Their enfliction of mouse SAT-box containing gene 17	NM_022454
shoughdipese A2, group M (cytosolie, calcium-independent)	035600_MM
Hypothetical protein PR02792	AF119898
moderateration (-1)	NH_COOOUTO
myoun tenang protein n hencefladest embain 51 (2009).	NH_017665
remedicin to the land of the l	XF332222
Productiful/Angelmen syndrome-5	AU118874
hypothetical protein TCBAP0738	AF283769
hant call factor (1 (MTG-accessory protein)	AA/03045
1900/2019 film navious world 1905/16 H= 310 316365-16 = 381 80 808 = 132 (South South Sout	100,000   March 100,000   Marc
ABBITION FIGURES OF ALL CONTRACTIONS ASSESS THAT A CONTRACT TO THE SOURCE OF THE SOURC	A£233437
myonowan related protein 3	NH_004826
medicio/menhold or mixed-inseque leutemia (trittoria homolog, Drosophila); translocated to, 4	NM_005936
cardlege esociated protein	NM_006371
serologically defined breast cancer antigen \$4	AF308298
butualities when finger probabilities EUROHIMAGE S66589	8,006148
O Matterna, farmity 3A	W93728
Terrain biding	A1803302
IQMON17 game product	A8007877
hypothetical protein FU11535	NM_024558
MENCENTY SECTION AND ACTIONS (Applies from the first contributions and proceedings).	ABU30.63
The section washington to the section of the sectio	NM 022559
metallicities at 1 (functional)	95217861
cytochrome P450, subtamily IIIA, potypoptible 7	S9/000_MM
Commences glockR02417; 1 (DEF=Homo sepiens cDNA FU1411 fs, chone MAMMA100150, FEA=mRNA (DB_XREF=gi:10436489 (MG=Hs, 288567 Homo sepiens cDNA FU14111 1A024173	5489 /UG=Hs.288567 Homa sapiens cDNA FLI14111 : AK024173
mensus includes gb.AK024129.1 /DEF¤Homo sapiens cONA FU14067 fis, clone HEMBB1001315. /FEA≖mRNA /DB_XREF≖gi:10436-	434 /UG=Hs.287619 Homo sapiens cDNA FLJ14067 f AX024129
XXN DNA binding protein	A936458
publishe 617-Sandrag protein strater to IAT/AAB10	ALOS/16/ AK02516
reportation provent risk two	NM_000163
GWCZ3 care arodod	AB011100
CONSTITUTE OF MACES 273.1 DEF = Nome supiers (DNA: FLIZ2620 fs, clone HS105629. FEL= mRNA //DB_JREF= gi:10439077 //JE= Hs. 306834 Home supiers (DNA: FLIZ2620 fs, clo AK026273	UG=Hs.306834 Homo sapiens cDNA: FLI22620 fis, clr AX026273
carbonic anhydrase IY	VH_000717
Consumes includes gb.A007119 /FEA=EST /OB_XREF=gr:3231455 /OB_XREF=est:0034405.x1 /CLOKE=IMAE;1639184 /UG=Hs.144339 Human DNA sequence from clone RP1-257A15 on A0017119	339 Kuman DNA sequence from clone RP1-257A15 or AI017119
Appellution protein MGZ656	505470_FMN
NOVEL SECTION A DEVELOPM 3	755500 RM
con your most reporture process. MEF = 0:25427.1 SEE = MAY (PRO) = protein-serinethronine lines (DB XREF = 0:405732 / I = 0:25427.1 SEE = REPERT   MEF = 0:405732 / I = 0:25427.1 SEE = REPERT   MEF = 0:405732 / I = 0:25427.1 SEE = 0:405732 / I = 0:40572 / I = 0:405	
pletante receptor, ionotropic, Lainate I	NM_000830
Consumes Includes gir. ALO19930.1 (DEF = Homa supiens mRNX, CDNA DKT 26566H201) (From clone DKT 2656H201). FEL=mRNX ADI, ZREF = gir.4500210 (WG=Hs. 302061 Homa sepiens m ALO199430	XREF=gi:4500210 /UG=Hs.302061 Homo sapiens m/ AL049430
MODAS7 protein	MM_021531
Come as No. 40 commit process (18 committee of 18 committee of	271717 ESTs. Weakh similar to ALU1 HUMAN ALU SUI BE378994
suborin 3, acids	NM_001839
to glucomytae (alphe glucosidae)	NM_004668
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naraparan 2, AIP-banding cassette, sub-laminy 5 (AUI/1/A)	SACION MA
the control of the second of t	4600755

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Man. L.A. Braham	******
Company there's march and the company that the company th	NM_003528
IDAN 1751 protein	
and bridges of 18748061 /FEA=EST /OB_XREF=gi:11295656 /OB_XREF=et:602022610F1 /CLONE=INAGE:4157907 /UG=Hs.167988 neural cell adhesion molecule 1	
- Jeli Hardy-Zuckerman 4 fefine sarroma viral encogene homolog	
hypothetical protein FU1 4803	BE619220
ATPase, Ca++ transporting, plasms membrane 2	X63575
DEAD/H (Jap-Gis-Na-Jap/Hs) box polypepide 34	AA039439
Hebiase phosphoprotein 10 (U3 small nudeolar ribonucleoprotein)	AL545921
DAVOromatin binding modif	NM_006618
idelinde coldase 1	NM_001159
Melend in accordants 4	AF248483
CONTRACTOR OF ANY 12056 FEATER 108 XXEF = 01:5631941 / OB XXEF = 01:708	n clone 1170K4 on chn A1912086
	BC004134
derete channel ( . stedetal musche (Thomsen disease, autosomal dominant)	NM_000083
History fusit, mentor	NM_003545
and the first (month of the first ) 450	113974
handleters overlein [F] 111 535	A1082827
designations extensive contracts	K03226
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UMORAL game product	1000 PM
ALMOST) protein	40055357
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EATA landing protein 1 (gloom traiscription factor 1)	A1920916
mynnine-gutamic and opposed (nt.) repeats	6974746
LANCE ADDITIONAL WILL PROPERTY OF THE PROPERTY	NA 004170
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the account (river area)	A8018740
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1933   Quantum Agrana agranged medical properties of the company o	NM 003635
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C LEGACIA DESCRIPTION OF THE CONTRACT OF THE C	AF001602
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Europhysical members 1	16Z500_NN
Comment includes the MIXTOOR 1 (DEE Home sensions ODA FLI (013) fits close HENBAI (03)441, FEA.m. MAY (08, XNEF-ac)702 1996, (MG-Hs, 274 128 Home sensions cDNA FLI (013) fits AKOOO993	ens cDNA FU10131 fis AK000993
4-Mai COS179   OFF Etherno sessions action derived transforming sequence (BLYH), mRNA, FEA=COS /GEN=BLYH /PROD=axion lymphoma virus-derived transformingseq NH_005179	rived transformings eq NM_005179
and the second section of the section of	NM_016280

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management of the control of the con	MSSERI	
ample of the second sec	NA 018422	3
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	5675311	44
Application to the contract of		5
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hearthalian action R110945	NM 018280	5
hrodynical protein [U135]	AK023573	1.45
HIS (-Ba (X. corwisiae)	AX024258	1.45
Conserva includes ob MOZ 4568, 1 DEF = Home sapiens (DNA: FU2091S fts, cone ADSE00692. FEA= mRNA /DB_MEF=qi:10436878 /UG=Hs. 306691 Home supiens cDNA: FU2091S fts,	15 fis, r AX024568	<u>.</u>
brain abandant, membrane attached signal protein 1		<u>=</u>
million 2	NM_012216	<u>-</u> .
cardinoendryonic entoen-retard cell adhesion molecule 7	NM_006890	<u>.</u>
PJAM1128 protein	A478879	<u>-</u>
a dainterarie lise and metallocordease (recroivein tree) with thrombos condin tree 1 molit. 8	NM_007037	4.
officers recents: large 1, such angle 2, suc	NM_002548	7
IMILEA control	8F516072	1
receive prouts receive of control is	AF030107	7
6A2-related on chromosome 22	Y07846	3.
erforthame A	NM_000487	7.
CTP binding protein 1	NM_004286	<u>-</u>
hypothetical protein from EURONHAEE 511235	NM_020147	<u>-</u>
dedicator of cyto-binesis 1	NM_001380	<u>-</u>
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